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protein search, using sw model

(without alignments) 1746.089 Million cell updates/sec US-09-328-877A-8 589 1 MSKPGKPTLNHGLVPVDLKS.....SRNGTEETKLLVLDFDVDMK 589 time 20.45 Seconds 412676 September 25, 2001, 14:42:05 ; Search Total number of hits satisfying chosen parameters: 412676 segs, 60623988 residues Post-processing: Listing first 45 summaries OLIGO Gapop 60.0 , Gapext 60.0 length: 0 length: 200000000 A\_Geneseq\_0601:\* 0 Minimum DB seq Maximum DB seq Title: Perfect score: Scoring table: Word size : OM protein •• Sequence: Searched: Run on:

/SIDS1/gcgdata/geneseg/geneseqp/AA1980.DAT:\* Database

- SIDS1/gcgdata/geneseq/geneseqp/AA1961.DAT:\*
   SIDS1/gcgdata/geneseq/geneseqp/AA1981.DAT:\*
   SIDS1/gcgdata/geneseq/geneseqp/AA1982.DAT:\*
   SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:\*
   SIDS1/gcgdata/geneseq/geneseqp/AA1985.DAT:\*
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- . DAT : /SIDS1/gcgdata/geneseq/geneseqp/AA1991. /SIDS1/gcgdata/geneseq/geneseqp/AA1992.
- /SID51/gcgdata/geneseq/geneseqp/AA1993.DAT /SID51/gcgdata/geneseq/geneseqp/AA1994.DAT /SID51/gcgdata/geneseq/geneseqp/AA1995.DAT /SID51/gcgdata/geneseq/geneseqp/AA1995.DAT DAT
- - ŝ
- DAT /SIDS1/gcgdata/geneseq/geneseqP/AA1997. /SIDS1/gcgdata/geneseq/geneseqP/AA1998.
  - DAT : 5
    - /SIDS1/gcgdata/geneseg/genesegp/AA1999.DAT

    - /SIDS1/gcgdata/geneseq/geneseqp/AA2000.DAT: /SIDS1/gcgdata/geneseq/geneseqp/AA2001.DAT: 21: 22:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Human mammary sel-	Human mammary sel-	Human mammary sel-	Human mammary sel-	Human GTPase assoc	Human hippocampal	Human mammary sel-	Human hippocampal	Human mammary sel-	Human hippocampal	
		•					,					
	ID	AAY22466	AAB59198	AAY22467	AAB59199	AAB01204	AAY 22465	AAY22468	AAB59197	AAB59200	AAY 22464	AAB59196
	DB	20	22	20	22	21	20	20	22	22	20	22
	Ouery Match Length DB ID	589	589	559	559	589	540	540	540	540	545	545
æ	Query Match	100.0	100.0	94.9	94.9	94.6	91.7	91.7	91.7	91.7	91.7	91.7
	Score	589	589	559	559	557	540	540	540	540	540	540
	Result No.		۲ ۲	m	4	ى ك	9	7	8	5	10	11

New isolated human sel-10 polypeptides

Li J, Pauley

Gurney ME,

WPI; 1999-458026/38. N-PSDB; AAX99702.

JS26820. 97US-0068243.

-0M86

17-DEC-1998; 19-DEC-1997;

01-JUL-1999.

Claim 24; Page 60-63; 91pp; English.

AAY22463 AAY22463 AAB59195 AAB59196 AAY22469 AAY22469 AAY22461 AAB59200 AAB59200 AAB59200 AAB59200 AAB59200 AAB59200 AAY221200 AAY221200 AAY221200 AAY321200 AAY321200 AAY321200 AAY321631 AAY321631 AAY321632 AAY321632 AAY321620 AAY321620 AAY366699 AAX866699 AAX866699 AAX66699 AAX866699 AAX866699 AAX866699	W18029
99997777770881015555555555555555555555555555	
00000000000000000000000000000000000000	
№ № № № № № № № № 4444444444444 600000000000000000000000	, & & & & &

Alpha chemokine GR MIP-Zalpha. Homo MIP-Zalpha. Homo

Human gro-beta che Human gro-gamma ch

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Human chemokine Human chemokine Human chemokine Human gro-alpha Protein used to

C-terminal mychis Human Cterm V5 his C-terminal V5 His Human secreted pro

Human C-term mychi

Amino acid sequenc Protein fragment e Human LYST2 polype Human LYST-2 prote

Mouse LYST2 polype

LYST-2

Human

prote

Human hippocampal Human 6myc-N-sel-1 Protein encoded by Human hippocampal Human hippocampal

hippocampal hippocampal hippocampal

Human Human Human



AAY22466 standard; Protein; 589 AA.

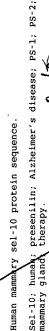
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AAY 22466 RESULT

(first entry)

29-SEP-1999

AAY22466



Homo sapiens.

W09932623-A1

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<pre>XX 23-MXY-2000; 2000WO-US09814. XX R 42-JUN-1999; 99US-0328877. FR 42-JUN-1999; 99US-0328877. FR 42-JUN-1999; 99US-0328877. Fr 7001-10240471. XX WPI; 2001-10240471. XX WPI; 2001-10240471. XX WPI; 2001-10240471. XX Fr 40 human sel-10 polyhoptides and their encoding polynucleotides, testing antipodies for detecting sel-10 polypeptide expression and as drug tangets in the treatment of Alzheimer's disease T expression and as drug tangets in the treatment of Alzheimer's disease T the present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raisinh monoclonal or polyclonal C antibodies useful in diagnostic assays for detecting sel-10 c angets for decreasing antibody levels in the treatment of Alzheimer's disease targets for decreasing antibodies are also useful as drug c targets for decreasing antibody levels in the treatment of Alzheimer's c argets for decreasing antibodies are also useful as drug c targets for decreasing antibody levels in the treatment of Alzheimer's c c argets for decreasing antibodies are also useful as drug</pre>	and Mate	1 MSKPGKPTLNHGLVPVDLKSAKEPLPHOTVMKIFSISIIAQGLPFCRRMKKLDHGSEV 	<pre>Db 121 kmfgswsgpekilaldeildsceptqvkhmmqviepqfqrdfisilpkelalyvisflep 180 Qy 181 kDLLOAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGFIHSPWKSAYIRQ 240                                     </pre>	Qy       361       RDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAVDFMVKVWDPFTETCLHTLQ       420         bb       361       IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
This sequence represents a human sel-10 protein of the invention. sequence is specifically a human mammary sel-10 protein. The polyperides can be used to alter presentiin function. Compounds which inhibit the expression or the activity of the human sel-10 polypeptides reverse the effects of mutations to presentiin-1 (ps-1) or ps-2, a therefore may be useful for the prevention or treatment of Alzhein disease. Sequence 589 AA; Sequence 589 AA; Juery Match 100.04; Score 589; DB 20; Length 589; Matches 589; Conservative 0; Mismatches 0; Indels 0; Ga Matches 589; Conservative 0; Mismatches 0; Indels 0; Ga 1 MSKPGKPTLNHGLVPVDLKSAKEPLPHOTVMKIFSIIIAQGLPFCRRNKKKDHGSEV 111111111111111111111111111111111111	<pre>Qy 121 KMFOSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLEP 180 11111111111111111111111111111111111</pre>	301 GHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHERRVVSGS 	421 481 481 541 541 541 541 80198 859198	D ABE59198 standard; protein; 589 AA. AC ABE59196 DE Human mammary sel-10-1 protein. XX 23-MAR-2001 ffirst entry) XX Sel-10; human; Alzhermer's disease; Abeta. XX W0200075328-A1. XX HODC -2000.

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qa	541 nlvtlesggsggvvwrirasntklvcavgsrngteetkllvldfdvdmk 589	Db 301 etgecihtlyghtstvrcmhlhekrvvsgsrdatlrvwdietgeclhvlmghvaavrevg 360
RES AAY ID	RESULT 3 AA122467 ID AAY22467 standard; Protein; 559 AA.	Qy         391         YDGRRVVSGAYDFMVKVMDPETETCLHTLQCHTNRVYSLQFDGIHVYSGSLDTSIRVMDV         450         111111111111111111111111111111111111
XXX	AAY22467;	
X E S	29-SEP-1999 (first entry)	
VE X	Human mammary sel-10 protein sequence.	QY 511 CLQFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGS 570
KW KW	Sel-10; human; presenilin; Alzheimer's disease; PS-1; PS-2; mammary gland; therapy.	Db 481 clqfnknfvitssddgtvklwdlktgefirnlytlesggsggvvwrirasntklycavgs 540
XX OS	Homo sapiens.	571 RNGTEETKLLVLDFDVDMK 58
N N N	W09932623-A1.	Db 541 rngteetkllvldfdvdmk 559
Xa	01-JUL-1999.	
XX FF	17-DEC-1998; 98WO-US26820.	AAB59199 ID AAB59199 standard; protein; 559 AA.
AX PR	19-DEC-1997; 97US-0068243.	AAB59199;
XX FA	(PHAA ) PHARMACIA & UPJOHN CO.	XX DT 23-MAR-2001 (first entry)
V I A	Gurney ME, Li J, Pauley AM;	(X DE Human mammary sel-10-2 protein.
X H H	WPI; 1999-458026/38. N-PSDB: AAX99702.	(X Vv Sel-10; human; Alzheimer's disease; Abeta.
XX	an sel-10 polybentides	X Homo sapiens.
XX	m Ji Dar 63-66, 01-00, East	W WO200075328-A1.
XX	CTATH \$4' FAGE 03-00' STPP; ENGLISH.	tx PD 14-DEC-2000.
ខ្លួនទ	This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human mammary sel-10 protein. The polypeptides	
ខេត	can be used to after presenting function. Compounds which initial either the expression of the activity of the human sel-10 polyperides may remove the effects of mutations to acconding 100-100-000 and 200-200-200-200-200-200-200-200-200-200	X 28 09-JUN-1999; 99US-0328B77.
ខេត	therefore may be useful for the prevention or treatment of Alzheimer's disease	X V (PHAA ) PHARMACIA & UPJOHN CO.
XX	Servience 550 AA.	JI Pauley AM, Gurney ME, Li J;
Š		XX WPI; 2001-102404/11.
OđŽ	Query Match 94.9%; Score 559; DB 20; Length 559; Best Local Similarity 100.0%; Pred. No. 0; Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	AN New human sel-10 polypeptides and their encoding polynucleotides, Pr useful for raising antibodies for detecting sel-10 polypeptide Pr expression and as drug targets in the treatment of Alzheimer's disease
οy d	31 MKIFSISIIAQGLPFCRRNKRKLDHGSEVRSFSLGKKPCKVSEYTSTJGLVPCSATPT 90 	yr - XX S Claim 1; Page 83-86; 116pp; English.
oy B	FGDLRAANGGOORRRITSVOPPTGLOEWLKMFOSSKSEPEKLLALDELIDSCEPTQVKHM 150 	CC The present invention relates to human sel-10. The sel-10 proteins of CC the invention are useful for raising monoclonal or polyclonal CC antibodies useful in diagnostic assays for detecting sel-10 CC nolveenide expression the sel-10 polyceenides are also useful as drun
οy	MOVIEDOFORDFISLLEPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDULLWREKCKEE 210	purpreture expression, the set to purpretures are approximate targets for decreasing antibody levels in the treatment of Alzheime disease. It is also useful for identifying agents capable of altering the uncloriton level verse whe molynumleantides are use
qq	ekckee 180	for deve with the
QY Db	<pre>211 GIDEPLHIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQ 270 111111111111111111111111111111111111</pre>	Sequ
Qγ	FCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIISGSTDRTLKVWNA	94.98; 100.08
q :	fcgnrivsgsddntlkvwsavtgkclrtlyghtggvwssqmrdniisgstdrtlkvwna 300	Match
δ	331 ETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQ 390	QY 31 MKIFSISIIAQGLPFCRRRMKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTT 90

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dd	 1 mkifs		
ло 40 Со 42	91 FGDLF	FGDLRAANGOGQQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHM 150	
-		1 5	
4			
0Y 21. Db 18.	1 GID       1 gid	<pre>EPLHIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQ 270                                     </pre>	
7	1 FCG	KVWNA 3	
7	41 fcgnr	nrivsgsddntlkvwsavtgkclrtlvghtggvwssqmrdniiisgstdrtlkvwna 300	
Qy 3; Db 3(	31 ETGEC       01 etgec	ETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQ 390 	
0y 39 Db 36	91 YDGRF       61 ydgrr	DGRRVVSGAYDFWVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDV 450 	
QY 45 Db 43	51 ETGNC       21 etgnc	ETGNCIHTLTGHQSLTSGMELKDNILVSGNaDSTVKIWDIKTGQCLQTLQGPNKHQSAVT 510 	
L	, ,		
0y 5.	11 CLQFN 11111 81 clqfn	LQFNKNFVITSSDDGTVKLMDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGS 570 	
OY 51 Db 54	71 RNGTE       41 rngte	RNGTEETKLLVLDFDVDMK 589                   rngteetkllvldfdvdmk 559	
RESULT IID AAB01204 XXX AAB01204 XXX AAB01204 XXX AAB01204 XXX AAB01 XXX AAB01 03 - NU DE Humau DE Humau XXX Guan XXX Guan XXX Guan XXX 03 - UT PPR 04 - FI PPR 05 - UT PPR 05	T 5 204 204 204 204 204 201204; 33-NOV-200 33-NOV-200 67Pase; G7 autoinmun autoinmun autoinmun autoinmun autoinmun autoinmun autoinmun autoinmun autoinmun 23-NOV-200 23-NOV-199 23-NOV-199 23-NOV-199 23-NOV-199 23-NOV-199 23-NOV-199 1411man JT	10; 10; 10; 10; 10; 10; 10; 10; 10; 10;	
PI Yan XX	д J,	Azimzal'Y;	

DR	WPI; 2000-400073/34. N-PSDB; AAA49199.	
X L L L L L L L L L L L L L L L L L L L	Human GTPase associated proteins, polynucleotides, and antibodies, useful for diagnosing, preventing and treating various diseases such as atherosclerosis, cancer, acquired immune deficiency syndrome (AIDS), asthma, and autoimmune diseases -	
XX PS	Claim 1; Page 118-120; 144pp; English.	
ខួនខួន	Human cDNA libraries from various tissues were screened for GTPase associated proteins (GTPAP). The present sequence is human	
ទទទ	GFAP-19 procent. This sequence was derived from a cown intrary of brain tunnour tissue. This protein is expressed in nervous, reproductive and gastrointestinal tissue. The GTPAP proteins may be	
ខខ	ě	
ខ្លួន	useful for treatment or prevention of diseases associated with GTPAP such as cell proliferation disorders, autoimmune disorders,	
ខខ	inflammatory disorders, immune system disorders, cancer, ALDS, asthma, atherosclerosis, arthritis, systemic lupus erythematosus and psoriasis.	
so	Sequence 589 AA;	
nö	ch 94.6%; Sco 54.6%; Sco	
Ma	es 557; Conservative (	
οy	33 IFSISIIAQGLPFCRRMKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFG 92 111111111111111111111111111111111111	
qq	33 ifsisiiaqqlpfcrrrmkrkldhgsevrsfslgkkpckvseytsttglvpcsatpttfg 92	
σλ	3 DERAANGOGOORRRITSVOPPTGLOEWLKMPQSWSGPEKLLALDELIDSCEPTOVKHMMQ 15	
qq	3 dlraanggggggrrritsvgpptglgewlkmtgswsgpekilaidelidsceptgvknmmg 15	
δ δ	153 VIEPOFORDFISLLPKELALVVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEG51 212 	
8		
5 8	3 deplhikrrkvikpgfihspwksayirqhridtnwrrgelkspkvlkghddhvitclqfc 27	
αy	273 GNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSQMRDNIIISGSTDRTLKVWNAET 332	
qq	273 gnrivsgsddntlkvwsavtgkcIrtlyghtggvwssqmrdnliisgstdrtlkvwnaet 332	
QY	333 GECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYD 392	
qq	333 gecihtiyghtstvrcmhlhekrvvsgsrdatlrvwdletgqclhvlmghvaavrcvqyd 392	
oy b	393 GRRVVSGAYDEMVKVWDPETETCLHTLOGHTNRVYSLOEDGIHVVSGSLDTSIRVWDVET 452 111111111111111111111111111111111111	
Qγ	453 GNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIMDINTGQCLQTLQGPNKHQSAVTCL 512	
qq	453 gncihtltghqsltsgmelkdnilvsgnadstvkiwdiktggclqtlqgpnkhqsavtcl 512	
оy	513 QENKNEVITSSDDGTVKLMDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRN 572	
qq	513 gfnknfvitssddgtvklwdlktgefirnlvtlesggsgggvvwrirasntklvcavgsrn 572	
QY	573 GTEETKLLVLDFDVDMK 589	
qq	573 gteetklividfavdmk 589	
RESU AAY2 ID	RESULT 6 AAY22465 ID AAY22465 standard; Protein; 540 AA.	

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XX AC AAY22465; VV	QY 470 ELKDNILVSGNADSTVKIMDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVK 529
or DT 29-SEP-1999 (first entry) VV	
ok DE Human hippocampal sel-10 protein sequence.	0Y 530 LWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDMK 589
xx xx Sel-10; human; presenilin; Alzheimer's disease; PS-1; PS-2; hippocampus; KW therapy.	Db 481 Ludiktefiniktiesggsggvvwrirasntklvcavgsrngteetklividfdvdmk 540
XX OS Homo sapiens.	RESULT 7
XX PN W09932623-A1. VV	AAY22468 ID AAY22468 standard; Protein; 540 AA.
01-JUL-1999.	XX AC AAY22468;
PF 17-DEC-1998; 98WO-US26820.	XX DT 29-SEP-1999 (first entry)
AR 19-DEC-1997; 97US-0068243. XX	XX DE Human mammary sel-10 protein sequence.
PA (PHAA) PHARMACIA & UPJOHN CO. XX	
FI Gurney ME, Li J, Pauley AM; vv	mammary gland;
AAA WPI; 1999-458026/38. Dr n-PSDB; AAX99701.	OS Homo sapiens. XX PN WOQ932623-A1
XX PT New isolated human sel-10 polypeptides	
XX PS Claim 24; Page 57-59; 91pp; Bnglish.	
This sequence represents a human sel-10 protein of the invent	XX PR 19-DEC-1997; 97US-0068243.
sequence is specifically a human hippocampal sel-10 protein. T polypeptides can be used to alter presentlin function. Compoun inthis other and be used to alter presentlin function.	XX PA (PHAA) PHARMACIA & UPJOHN CO.
C further expression of the activity of the human set.10 C polypeptides may reverse the effects of mutations to presentin-1 (PS-1) C or PS-2, and therefore may be useful for the monostic of transmost of	-
Alzheimer's disease.	XX DR WPI; 1999-458026/38. DP N-DEND. AXY09707
5Q Sequence 540 AA;	
Query Match 91.7%; Score 540; DB 20; Length 540; Best Local Similarity 100 0%; Dread No. 0.	_
0; Conservative 0; Mismatch	
DY 50 MKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGGGQQRRRITS 109 11111111111111111111111111111111111	CC sequence is specifically a human mammary sel-10 protein. The polypeprides CC can be used to alter presentin function. Compounds which inhibit either CC the expression or the activity of the human sel-10 polypeprides may CC reverse the effects of mutations to presentin-1 (PS-1) or PS-2, and
2Y 110 VQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKE 169 11111111111111111111111111111111111	
<pre>170 LALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRKYIK                                    </pre>	atch 91.7%; Score 540; DB 20; Length 540; cal Similarity 100.0%; Pred. No. 0;
2) 230 HSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWS 289 111111111111111111111111111111111111	<pre>Matches 540; Conservative 0; Mismatches 0; Indels 0; Ga 50 MKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITS                                     </pre>
Oy290AVTGKCLRTLVGHTGGVWSSOMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCM34911111111111111111111111111111111111	1 mkrkldhgsevrsfslgkkpckvseytsttglvpcsatpttfgdlraangggggrrrits 110 vQPP7GLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFORDFISLLPKE 
2Y 350 HLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWD 409 111111111111111111111111111111111111	
410 361	Db 121 lalyvlsflepkdllqaaqtcrywrilaednllwrekckeegideplhikrrkvikjgfi 180 Qy 230 HSPWKSAYIRQHRIDTNWRRGELKSFKVLKGHDHVITCLQFCGNRIVSGSDDNTLKVWS 289 

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181 hspwksayirghridtnwrrgelkspkvlkghddhvitclqfcgnrivsgsddntlkvws 240	Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps
290 AVTGKCLRTLVGHTGGVMSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCM 349 	Qy         50         MKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITS         10           1         111111111111111111111111111111111111
HLHEKRVVSGSRDATLEVWDIETGOCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWD 4	110 VQPPTGLQEWLKMFQSWSGPEKLLALDELIDSGEPTQVKHMMQVIEPQFQRDF1SLLFKE 
hlhekrvvsgsrdatlrvwdietgqclhvlmghvaavrcvqydgrrvvsgayd	Db 61 vqpptglqewlkmfqswsgpekllaldelidsceptqvkhmmqviepqfqrdfisllpke 120
<pre>410 PETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGM 469 111111111111111111111111111111111111</pre>	Qy       170       LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGF1       229         111111111111111111111111111111111111
470 ELKDNILVSGNADSTVKIWDIKTGQCLQTLQGFNKHQSAVTCLQFNKNFVITSSDDGTVK 529 	Qy       230       HSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWS       28         111111111111111111111111111111111111
530 LWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDMK 589 	QY 290 AVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCM 349 
	QY 350 HLHEKRVVSGSRDATLRVWDIETGOCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWD 409 111111111111111111111111111111111111
AAB59197; Staudatu; Protein; 340 AA. AAB59197;	410 PETETCLHTLOGHTNRVYSLOFDGTHVVSGSLDTSTRVWDVETGNCTHTLTGHOSLTSGM
23-MAR-2001 (first entry)	α τος
Human hippocampal sel-10-5 protein.	OY 470 ELKDNILVSGNADSTVKIMDIKTGQCLQTLQGPNKHQSAVTCLQFNKHVITSSDDGTVK 52 1
Sel-10; human; Alzheimer's disease; Abeta.	5 10 LWDLKTGEFIRNLVTLESGGGGGGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDGVG9777
Homo sapiens.	<pre>111111111111111111111111111111111111</pre>
WO200075328-A1.	***************************************
14-DEC-2000.	RESULT 9 AARSO200
23-MAY-2000; 2000WO-US09814.	ID AAB59200 standard; protein; 540 AA. xx
09-JUN-1999; 99US-0328877.	AC AAB59200;
(PHAA ) PHARMACIA & UPJOHN CO.	DT 23-MAR-2001 (first entry) xx
Pauley AM, Gurney ME, Li J;	DE Human mammary sel-10-3 protein. xx
WPI; 2001-102404/11.	KW Sel-10; human; Alzheimer's disease; Abeta. XX
New human sel-10 polypeptides and their encoding polynucleotides, neaful for raising antihodies for detection solution polynomials	OS Homo sapiens.
in the treatment of Alzheimer'	PN W0200075328-A1.
rietm 1. Door 75.700 116mm. Emolich	PD 14-DEC-2000.
040 10	PF 23-MAY-2000; 2000WO-US09814.
the present invention retaces to nummi ser iv. The set iv proteins of the invention are useful for raising monoclonal or polyclonal	PR 09-JUN-1999; 99US-0328877.
eful as dr	AA (PHAA ) PHARMACIA & UPJOHN CO.
	PI Pauley AM, Gurney ME, Li J;
allering the production level of Abeta, the polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological mathemat that lead to blockmort's discase	WPI; 2001-
	PT New human sel-10 polypeptides and their encoding polynucleotides, PT useful for raising antibodies for detecting sel-10 polypeptide PT expression and as drug targets in the treatment of Alzheimer's disea
Query Match 91.7%; Score 540; DB 22; Length 540; Best Local Similarity 100.0%; Pred. No. 0;	VI - XX PS Claim 1; Page 86-89; 116pp; English.

Claim 1; Page 86-89; 116pp; English.

91.7%; Score 540; DB 22; Length 540; 100.0%; Pred. No. 0;

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<pre>XX FF 17-DEC-1998; 98WO-US26820. XX 19-DEC-1997; 97US-0068243. FHAA ) PHARWACIA &amp; UPJOHN CO. Gurney ME, Li J, Pauley AM; WPI; 1999-458026/38 WPI; 1900-458026/38 WPI; 1990-458026/38 WPI; 1990-458026/38 WPI; 1990-458026/38 WPI; 1990-458026/38 WPI; 1990-458026/38 WPI; 1990-458026/38 WPI; 1990-458026/38 WPI; 1990-458026/38 WPI; 1990-478026/38 WPI; 1990-478026/38</pre>	Query Match91.7%; Score 540; DB 20; Length 545; Best Local Similarity 100.0%; Pred. No. 0; Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 07 50 MKRKLDHGSEVRSFSLGKKPCKVSEYTSTGLVPCSATPTFGDLAANGGGORRRITS 109 111111111111111111111111111111111111	Qy410PETETCLHTLÖGHTNRVYSLOPDCIHVVSGSLDTSIRVMDVETGNCIHTLFGHQSLTSGM 469Db366Petetclhtlqghtnrvyslqfdgjhvvsgsldtsirvwdvetgncihtlyhqsltsgm 425Qy470ELKDNILVSGNADSTVKLWDIKTGQCLQTLQGPNKHQSAVTCLQPNKNFVITSSDGTVK 529Qy470ELKDNILVSGNADSTVKLWDIKTGQCLQTLQGPNKHQSAVTCLQPNKNFVITSSDGTVK 529Qy470ELKDNILVSGNADSTVKLWDIKTGQCLQTLQGPNKHQSAVTCLQPNKNFVITSSDGTVK 529Qy530LWDLKTGEFIRNLVTLESGGSGGVVWRIPASNTKLVCAVGSRNGTEETKLLVLDFDVDMK 589Qy530LWDLKTGEFIRNLVTLESGGSGGVVWRIPASNTKLVCAVGSRNGTEETKLLVLDFDVDMK 589Db486LWdlktgefirnlvtlesggsggvvwrirasntklvcavgsrngteetkllvldfdvdmk 545RESULT1111AB59196Standard; protein; 545 AA.XXAAB59196;XAB59196;
The present invention relates to human sel-10. The sel-10 proteins the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as targets for decreasing antibody levels in the treatment of Alzheim disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are us for developing assays for identifying agents capable of interferin with the biological pathways that lead to Alzheimer's disease. Sequence 540 AA; Sequence 540 AA; Matches 540; conservative 0; Mismatches 0; Indels 0; Ga Matches 540; conservative 0; Mismatches 0; Indels 0; Ga for Matches 540; conservative 0; Mismatches 0; Indels 0; Ga Matches 540; conservative 0; Mismatches 0; Indels 0; Ga for WithIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	<ul> <li>OY 170 LALYLEFLERADILGAAOTCRYMRILAEDNLLWREKCKEGEGIDEPLHIKRKWYLKPGET 229</li> <li>DD 121 111/11111111111111111111111111111</li></ul>	RESULT 10 AAY22464 standard; Protein; 545 AA. XX AC AAY22464 standard; Protein; 545 AA. AC AAY22464 standard; Protein; 545 AA. AC AAY22464; XX 29-SEP-1999 (first entry) XY BE Human hippocampal sel-10 protein sequence. XX Sel-10; human; presenilin; Alzheimer's disease; PS-1; PS-2; hippocampus; XX KW therapy. XX COS Homo sapiens. XX M09932623-A1. XX M09932623-A1. XX PD 01-JUL-1999.

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XX	Db 366 peteclhtlaghtnrvyslafdathvysasldtsirvwdvetancihtitahasltsam 425
DT 23-MAR-2001 (first entry) xy	
DE Human hippocampal sel-10-4 protein.	
XX XW Sel-10; human; Alzheimer's disease; Abeta.	426 elkdnilvsgnadstvkiwdiktggclqtlggpnkhqsavtclqtnknivitssddgtvk
XX OS Homo sapiens.	530 LWDLKTGEFIRNLVTLESGGSGSGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDMK 58 
XX PN WO200075328-A1.	Db 486 lwdlktgefirnlvtlesggsggvvwrirasntklvcavgsrngteetkllvldfdvdmk 545
XX PD 14-DEC-2000.	RESULT 12
XX PF 23-MAY-2000; 2000WO-US09B14.	AAY22463 ID AAY22463 standard; Protein; 553 AA.
XX PR 09-JUN-1999; 99US-0328877.	XX AC AAY22463;
XX PA (PHAA ) PHARMACIA & UPJOHN CO.	XX DT 29-SEP-1999 (first entry)
XX PI Pauley AM, Gurney ME, Li J;	XX DE Human hippocampal sel-10 protein sequence.
XX DR WPI; 2001-102404/11.	
XX PT New human sel-10 polypeptides and their encoding polynucleotides, PT useful for raising antibodies for detecting sel-10 polypeptide	KW therapy. XX Homo sapiens. OS Homo sapiens.
expression and as drug targets in -	
XX PS Claim 1; Page 72-75; 116pp; English.	
	XX PF 17-DEC-1998; 98WO-US26820.
the invention are useful for raising monocional or polycional antibodies useful in diagnostic assays for detecting sel-10	XX PR 19-DEC-1997; 97US-0068243.
	XX PA (PHAA ) PHARMACIA & UPJOHN CO.
discase. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides ar	XX PI Gurney ME, Li J, Pauley AM;
CC for developing assays for identifying agents capable of interfering XX with the biological pathways that lead to Alzheimer's disease.	XX DR WPI; 1999-458026/38. DR N-PSDB: AAX93701.
SQ Sequence 545 AA;	
91.7%; Score 540;	
LOCAL SIMILATILY IV. US; Nes 540; Conservative	¥88
	CC sequence is specifically a numan hippocampal set-10 protein. The CC polypeptides can be used to alter presentiin function. Compounds which CC inhibit either the expression or the activity of the human set-10
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<pre>66 vgpptglqewlkmfqswsgpekllaldelidsceptqvkhmmqviepqfqrdfisllpke</pre>	
Qy         170         LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGFI         229           DD         126         111111111111111111111111111111111111	Query Match 91.7%; Score 540; DB 20; Length 553; Rest Toral Similarity 100.0%; Pred No. 0;
230 HSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWS 1	Matches 540;       Conservative       0;       Mismatches       0;       Gaps       0;         Qy       50       MKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQQRRRITS       109
186 hspwksayirqhridtnwrrgelkspkvlkghddhvitciqfcgnrivsgsddntlkvws	Db 14 mkrkldhgsevrsfsigkkpckvseytsttglvpcsatpttfgdlraangggggrrrits 73
<pre>UV 290 AVTGKCLFTLVGHTGGVWSSQMRDMIIISGSTDRTLKVWARETGECHTLTCHTSTVRCM 349 111111111111111111111111111111111111</pre>	QY 110 VOPPTGLOGWLKMPOSWSGPEKLLALDELLDSCEPTOVKHMMQVIEPQFQRDFISLLPKE 169
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	QV 230 HSPWKSAYIROHRIDTNWRRGELKSPKVLKGHDBHVITCLOFCGNRIVSGSDDNTLKVWS 289

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<pre>Best Local Similarity 100.0%; Pred. No. 0; Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0 OY 50 MKRLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSÄTPTTFGDLRAANGGGOQRRRITS 109 11                                  </pre>	Qy     110     VOPPTGLOEWLKMFQSWSGFEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKE     169       01     1	Qy 170 LALYULSFLEPKDLLQAAQTCRYWRILAEDNLLMREKCKEEDGIDEPLHIKRRKVIKPGFI 229 	Qy 230 HSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDHVITCLQFCGNRIVSGSDDNTLKVWS 289 	Qy     290     AVTGKCLRTLVGHTGGVWSSQMEDNIILSGSTDRTLKVWNAETGECIHTLYGHTSFVRCM     349       111111111111111111111111111111111111	<ul> <li>Qy 350 HLHEKRVVSGSRDATLRVWDIETGOCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWD 409</li> <li>1                                    </li></ul>	Oy         410         PETETCLHTLQGHTNRVYSLOFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGM         469         111111111111111111111111111111111111	470 ELKDNILUSGNADSTVKIMDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVK 5 111111111111111111111111111111111111	Db 434 elkdnilvsgnadstvkiwdiktggclqtlggpnkhqsavtclqfnknfvitssddgtvk 493 Qy 530 LWDLKTGEFIRNLVTLESGGSGGVVWRIPASNTKLVCAVGSRNGTEETKLLVLDFDVDMK 589	Db 494 lwdiktgefinivtlesggsggvwrirasntkivcavgsrngteetklivldfdvdmk 53	RESULT 14	AAYZ2462 standard; Protein; 592 AA. V	AX AC AAY22462;	AA DT 29-SEP-1999 (first entry) XX	DE Human hippocampal sel-10 protein sequence. XX	<pre>KW Sel-10; human; presenilin; Alzheimer's disease; PS-1; PS-2; hippocampus; KW theravy.</pre>	XX OS Homo sapiens. XX PN W09932623-A1.		АХ РF 17-DEC-1998; 98WO-US26820. XX DD 10-DEC-1007. 07HS-0A69243	(PHAA ) PHARMAC	Gurney	DR WPI; 1999-458026/38. DR N-PSDB; AAX99701.		AA PS Claim 24; Page 47-50; 91pp; English.
<pre>{</pre>	QY 350 HLHEKRVVSGSRDATLRVMDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKWWD 409 	<pre>Qy 410 PETERCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLrGHQSLTSGM 469                                     </pre>	<pre>Qy 470 ELKDNILVSGNADSTVKIMDIKTGOCLQTLQGPNKHQSAVFCLQFNKNFVITSSDDGTVK 529 111111111111111111111111111111111111</pre>	<pre>Qy 530 LWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDMK 589 1                                    </pre>	SULT 13 559195	ID AABS9195 standard; protein; 553 AA. XX AC AAB59195; XX	DT 23-MAR-2001 (first entry) XX DE Human hippocampal sel-10-3 protein.	XX KW Sel-10; human; Alzheimer's disease; Abeta. XX		XX PD 14-DEC-2000. VX	AA PF 23-MAY-2000; 2000WO-US09814.	AA PR 09-JUN-1999; 99US-0328877. VV	AA (PHAA ) PHARMACIA & UPJOHN CO. XX	PI Pauley AM, Gurney ME, Li J; XX	DR WPI; 2001-102404/11. XX	PT New human sel-10 polypeptides and their encoding polynucleotides, PT useful for raising antibodies for detecting sel-10 polypeptide PT expression and as drug targets in the treatment of Alzheimer's disease PT -	XX PS Claim 1; Page 68-71; 116pp; English.	CC The present invention relates to human sel-10. The sel-10 proteins of CC the invention are useful for raising monoclonal or polyclonal CC antibudies useful in disconseries accuse for deposition colled				SQ Sequence 553 AA;	Query Match 91.7%; Score 540; DB 22; Length 553;

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<pre>PR 09-JUN-1999; 99US-0328877. X (PHAA ) PHARWACIA &amp; UPJOHN CO. Y Pauley AM, Gurney ME, Li J; Pauley AM, Gurney ME, Li J; WPI; 2001-102404/11. New human sel-10 polypeptides and their encoding polynucleotides, restul for raising antibodies for detecting sel-10 polypeptide PT expression and as drug targets in the treatment of Alzheimer's disease PT expression and as drug targets in the treatment of Alzheimer's disease PT expression and as drug targets in the treatment of Alzheimer's disease PT expression and as drug targets in the treatment of Alzheimer's disease PT expression and as drug targets in the treatment of Alzheimer's disease PT expression and as drug targets in the treatment of Alzheimer's disease PT expression. The sel-10 polypeptides are also useful as drug CC disease. It is also useful for fashing monoclonal or polyclonal antibodies useful for fashing monoclonal or polyclonal antibodies useful for fashing monoclonal or polyclonal CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of CC disease. It is also useful for identifying agents capable of interfering CC disease. It is also useful for identifying agents capable of interfering CC disease. It is also useful for identifying agents capable of interfering CC disease. It is also useful for identifying agents capab</pre>	Ouery Match         91.7%: Score 540: DB 22: Length 592: Best Local Similarity 100.0%; Pred. No. 0; Matches 540: Conservative 0; Mismatches 0: Indels 0; Gaps         0           Rest Local Similarity 110:000; Pred. No. 0; Matches 540: Conservative 0; Mismatches 0; Indels 0; Gaps         0;         53           Rest Local Similarity 111:000; Pred. No. 0;         0;         1000; Similarity 0;         0;         Gaps         Gaps         10;	Net 209 sec
<pre>XX CC This sequence represents a human sel-10 protein of the invention. This CC sequence is specifically a human hippocampal sel-10 protein. The CC polypeptides can be used to alter presentin function. Compounds which CC polypeptides may reverse the effects of mutations to presentine 1 CC polypeptides may reverse the effects of mutations to presentine 1 CC or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's disease. CC or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's disease. CC or PS-2, and therefore may be useful for the prevention or treatment of CC or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's disease. CC or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's disease. CC or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's disease. Ouery Match 91.7%; Score 540; DB 20; Length 592; Best Local similarity 100.0%; Pred. No. 0; Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 540; Conservative 0; Mismatches 0; Indels 0; Gaps 10; D 53 mtklidhgsevrsfigkkpckvseytstugivpcsatpttfgdiraangggggrrrits 112 OY 10 VOPFTGLOBWIKMFOSWSGPEKLIALDELIDSCEPPOVHHMOVIEDGFORDENTINFEK 169 11111111111111111111111111111111111</pre>	<pre>1/3 latyutstrepKdllqaaqCcrywrlLaednlLWrekKeegldepLhLKrrkvkpgHl 20 HSPWKSAYTROHRIDTWWRGEKKSFWVLKGhDHVTTCLQFCGNRTVSGSDNTLKVWS 29 AVTGKCLFTLVGHTGGVWSSQMBNUIISGSTDFTLKVWABETGECHFTLYGHTSVPKN 29 AVTGKCLFTLVGHTGGVWSSQMBNUIISGSTDFTLKVWABETGECHFTLYGHTSVPKN 29 AVTGKCLFTLVGHTGGVWSSQMBNUIISGSTDFLKVWABETGECHFTLYGHTSVPKN 29 AVTGKCLFTLVGHTGGVWSSQMBNUIISGSTDFLKVWABETGECHFTLYGHTSVPKN 20 HLHKRVVSGSENDATCRVDIETGGCLHVLMGHVAAVCCQYDGRRVVSGAYDFWVWW 20 HLHKKVVSGSENDATCRVDIETGGCLHVUNGHVAAVCCQYDGRRVVSGAYDFTWKW 20 HLHKRVVSGSENDATCRVDIETGGCLHVUNGHVAAVCCQYDGRRVVSGAYDFWVWD 20 HLHKRVVSGSENDATCRVDIETGGCLHVUSGHVAAVCCQYDGRRVVSGAYDFTSKGA 20 hLHKRVVSGSENDATCRVDIETGGCLHVUSGHVAAVCCQYDGRRVVSGAYDFTSKGA 20 hLHKRVVSGSENDATCRVDIETGGCLHVUSGHVAAVCCQYDGRRVVSGASDFTVK 20 hLHKRVVSGSENDATCRVDIETGGCLHVUSGHVAAVCCQYDGRRVVSGASDFTVSGA 20 hLHKRVVSGSENDATCRVDIETGGCLHVUSGHVAAVCCQYDGRRVVSGASDFTVSGA 20 hLHKRVVSGSENDATCRVDIETGGCLHVUSGHVAAVCCQYDGRRVVSGASDFTVSGA 20 hLHKVVSGSENDATCRVDIETGGCLHVUSGKLDYSSDGTV 21 h11111111111111111111111111111111111</pre>	PF 23-MAY-2000; 2000WO-US09814. XX

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Sequence 3, Appli Sequence 4, Appli Sequence 2, Appli Sequence 3, Appli	40		Sequence 7, Appli Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli	- 41	S,																Length 209; ); Indels 0; Gaps 0;	
.4 73 .4 73 .4 73 .4 73	8 1.4 73 3 8 1.4 73 5	8 1.4 73 5 8 1.4 73 5 8 1.4 106 1 8 1.4 106 2	8 1.4 106 2 8 1.4 106 3 8 1.4 106 5 8 1.4 107 1	8 1.4 107 1 8 1.4 107 2 8 1.4 107 2	8 1.4 107 2	ALIGNMENTS		RESULT 1 US-08-899-578-6 ; Sequence 6, Application US/08899578	; Patent No. 6087153 ; GENERAL INFORMATION:	APPLICANT: Greenwald, Iva APPLICANT: Hubbard, E. Jane APPLICANT: Hubbard, E. Jane NUMBER OF INVERTION: SEL-10 AND USES THEREOF NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSEE: COOPER & Dunham LLP STREET: 1145 Avenue of the Americas CITY: New York	; STATE: New York ; COUNTRY: U.S.A. ; ZIP: 1036 ; COMPUTER READABLE FORM:	<pre>MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30 </pre>	<pre>; CURRENT APPLICATION DATA: ; APPLICATION NUMBER: US/08/899,578</pre>	FILING DATE: 24-JUL-1997 FILING DATE: 24-JUL-1997 CLASSIFICATION: 435 ATTORNEY/AGENT INFORMATION: NAME: White, John P.	REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 0575/53200/JFW/AKC	TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400 TETERX: /213) 778-6455	FOR	; LENGTH: 209 amino acids ; TYPE: amino acid	; STRANDEDNESS: single ; TOPOLOGY: linear ; MCLECULT TYPE: peotide		Query Match 2.0%; Score 12; DB 3; Lenc Best Local Similarity 100.0%; Pred. No. 0.0016; Matches 12; Conservative 0; Mismatches 0; 1	Qy 438 SGSLDTSTRVWD 449             Db 139 SGSLDTSTRVWD 150
Ltd.		h time 13.51 Seconds t alignments) Million cell updates/sec	SRNGTEETKLLVLDFDVDMK 589				197339			* * * * * Personal Pe	y chance to have a le result being printed, distribution.		g	0000	0 in	.46	m`	e 19 6 19	Sequence 20, Appl Sequence 18, Appl Sequence 19, Appl	0, 20 0, 20 0, 20		sequence 4, Appl1 Sequence 26, Appl Sequence 27, Appl Sequence 28, Appl Sequence 2, Appli
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen	cein search, using sw model	September 25, 2001, 14:43:40 ; Search (without 897.684 h	US-09-328-877A-8 589 1 MSKPGKPTLNHGLVPVDLKSSRNG7	OLIGO Gapop 60.0 , Gapext 60.0	197339 seqs, 20590346 residues	0	hits satisfying chosen parameters:	length: 0 length: 200000000	Listing first 45 summaries	<pre>Issued_Patents_AA:*</pre>	s the number of results predicted by ar than or equal to the score of the yed by analysis of the total score d	ac	Length DB	~~~~	×	.4 16 1 .4 37 3 .4 37 3	4 73 1 4 73 1	.4 73 1 .4 73 1	.4 /3 L .4 73 1 .4 73 1		~~~	1.4 7.3 1 05-08-485-111-4 1.4 7.3 2 05-08-436-420-26 1.4 7.3 2 05-08-436-420-27 1.4 7.3 2 05-08-436-420-28 1.4 7.3 3 05-08-846-966-2
	OM protein – protein	Run on:	Title: Perfect score: Sequence:	Scoring table: (	Searched:	Word size : (	Total number of hi	Minimum DB seq ler Maximum DB seq ler	Post-processing: Listing	Database :	Pred. No. 15 score greate and is deriv	Result OL	score	1 12 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8								

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RESULT 2 US-08-899-578-2 US-08-899-578-2 Sequence 2, Application US/08899578 Patent No. 6087133 GENERAL INFORMATION: APPLICANT: Hubbard, E. Jane APPLICANT: HUBbard, E. Jane APPLICANTE: New York CORRESPONDENCE ADDRESS: ADDRESSEE: COOPER'S 7 CORRESPONDENCE ADDRESS: ADDRESSEE: COOPER'S 7 CORRESPONDENCE ADDRESS: STRATE: New York COUTY: U.S.A. ZIP: 10036 COMPUTER READABLE FORM: MEDLIN TYPE: FLOPPY disk COMPUTER READABLE FORM: MEDLIN TYPE: FLOPPY disk COMPUTER READABLE FORM: MEDLIN TYPE: PATENTIN RELEASE #1 CORRENTING SYSTEM: PATAN SOFTWARE: PATENTON NUMBER: US/08/099 FILING DATE: 24-JUL-1997 FILING DATE: ADDALE. ATORNEY/AGENT INFORMATION: ANDE: WAME: WAME, JOHN P.	REGISTRATION NUMBER: 28,678 RESENCE/DOCKET NUMBER: 0575 TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400 TELEFAX: (212) 278-0400 TELEFAX: (212) 278-0400 SECUENCE CHARACTERISTICS: LENGTH: 587 amino acid TOPOLACE: amino acid TTYPE: amino acid TOPOLACE: 11near NOLECULE TYPE: protein US-08-899-578-2 Query Match Best Loal Similarity 100,0%; Pr Best Loal Similarity 100,0%; Pr Best Loal Similarity 100,0%; Pr Matches 12; Conservative 0; Matches 12; Conservative 0; Db 435 SGSLDTSIRVWD 446	RESULT 3 US-08-671-094B-3 Sequence 3, Application US/08671094B Factent No. 591232 GENERAL INFORMATION: APPLICAWT: Talmadge, James E. TTILE OF INVENTION: Anti-inflammator TTILE OF INVENTION: Anti-inflammator CONDATE: PALICATION DATA: CURRENT APPLICATION DATA:

STRANDEDNESS: not relevant TOPOLOGY: not relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO	Query Match 1.4%; Score %; DB 2; Length 14; Best Local Similarity 100.0%; Pred. No. 0.81; Matches %; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ANTI-SENSE: NO FEATURE: NO MAME/KEY: Modified-site LOCATION: 46 COMPED TARDAMATION: Anthen TWAN ANATOMIA	QY 494 QCLQTLQG 501         Db 3 QCLQTLQG 10
OTHER INFORMATION: ADDRESS THE CYSTELLE LESLUES OTHER INFORMATION: may be substituted with aminobutyric acid, homocysteine, or OTHER INFORMATION: diaminosuberic acid." -08-671-094B-5	RESULT 6 US-00-311-307B-6 ; Sequence 6, Application US/08311307B ; Patent No. 5627156
Query Match 1.4%; Score 8; DB 2; Length 13; Best Local Similarity 100.0%; Pred. No. 0.76; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	GENERAL INFORMATION: APPLICANT: TAImadge, James E. TITLE OF INVENTION: Polypeptide Agonist Derived From Human TITLE OF INVENTION: Interleukin-8
494 QCLQTLQG 501          3 QCLQTLQG 10	<pre>&gt;&gt; NUMBER OF SEQUENCES: 12 &gt;&gt; CORRESPONDENCE ADDRESS: &gt;&gt; ADDRESSEE: Dann, Dorfman, Herrell and Skillman &gt;&gt; STREET: 1601 Market Street &gt;&gt; CITY: Philadelphia</pre>
RESULT 5 US-08-671-094B-2 ; Sequence 2, Application US/08671094B : Patent No. 5912312	STATE: PA STATE: PA 2 CUNTRY: USA 2 CONTTER READALE FORM: 2 CONTTER READALE FORM:
GENERAL INFORMATION: APPLICANT: Talmadge, James E. TITLE OF INVENTION: Anti-inflammatory Polypeptide TITLE OF INVENTION: Antaconists of Winner Interlevien-R	<pre>converter fighty disk compatible convertible conv</pre>
NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSEB: Dann, Dorfman, Herrell and Skillman STRPERT: 1601 Market Stroot	PURCENTION NUMBER 105/08/311,307B FILING DATE: 23-SEP-1994 CLASSIFICATION: 514
CITY: Philadelphia STATE: PA COUNTRY: USA	ATTORNEL/MAGENT INFORMATION: NAME: Hagon, Patrick J. REGISTRATION NUMBER: 27,643 REFERENCE/DOCKET NUMBER: 6306
E A G	TELECOMMUNICATION INFORMATION: TELEBHONE: (215)553-4100 TELEFAX: (215)555-4044
COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30	бшн
CURKENT APPLICATION DATA: APPLICATION NUMBER: US/08/671,094B FILING DATE: 28-JUN-1996 CLASSTEPTON: 514	TYPE: amino acid STRANDEDNESS: not relevant TOPLOGY: not relevant
ATTORNEY/AGENT INFORMATION: NAME: Hagan, Patrick J. Refistration Nimere - 77.643	MULECULE TIPE: PEPLICE HYPOTHETICAL: NO ANTI-SENSE: NO
REFERENCE/DOCKET NUMBER: 63086FWC TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION:	ified- 6
TELEFANNES: (215)305-4100 TELEFAX: (215)563-4044 INFORMATION FOR SEQ ID NO: 2: SEDIFACE CHARAMERICATCS:	OTHER INFORM OTHER INFORM OTHER INFORM
LENGTH: 14 amino acids TYPE: amino acids	
ÖÖür	Query Match 1.4%; Score 8; DB 1; Length 15; Best Local Similarity 100.0%; Pred. No. 0.86; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
ANT.TELETORE. NO FEATURE: NAME/KEY: Modified-site	QY 494 QCLQTLQG 501 .         Db 5 QCLQTLQG 12
LOCATION: 46 OTHER INFORMATION: /note= "The cysteine residues OTHER INFORMATION: may be substituted with aminobutyric acid, homocysteine, or OTHER INFORMATION: diaminosuberic acid." -08-671-094B-2	RESULT 7 US-Q8-311-307B-3 ; Sequence 3, Application US/O8311307B ; Patent No. 5627156 ; GENERAL INFORMATION:

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/note- "The cysteine residues may be substituted with aminobutyric acid, homocysteine or diaminosuberic acid." ö Gaps BSULT BESULT US-08-476-376-12 Sequence 12, Application US/08476376 Patent No. 6103234 Betent No. 6103234 CENERAL INFORMATION: REPLICANT: CERAMI, ANTHONY APPLICANT: CERAMI, ANTHONY APPLICANT: SHERRY, BARBARA APPLICANT: SHERRY, SHERRY, SHERRY, SHERRY, SHERT, FLOOR STREFT: ö 0; Indels 1.4%; Score 8; DB 1; Length 16; 100.0%; Pred. No. 0.91; tive 0; Mismatches 0; Indels COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PALENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA: SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: TELEBORNEL APPLICATION NUMBER: US/08/311,307B FILING DATE: 23-SEP-1994 CLASSIFICATION NUMBER: US/08/311,307B ATTORNEY/GENT INFORMATION: NAME: Hagan, Patrick J. ATTORNEY/GENT INFORMATION: NAME: Hagan, Patrick J. ATTORNEY/GENT INFORMATION: TELEPHONE: (215)563-4104 TELEPHONE: (215)563-4104 INFORMATION FOR SEQ 1D NO: 4: SEQUENCE CHARACTERISITICS: LENGTH: 16 amino acids PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/285,498 APPLICATION NUMBER: US 08/285,498 PRILIG DATE: 03-AUG-1994 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/476,376 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435 PC-DOS/MS-DOS TYPE: amino acid STRANDEDNESS: not relevant TOPOLOGY: not relevant NAME/KEY: Modified-site Query Match 1.4 Best Local Similarity 100. Matches 8; Conservative TOPOLOGY: not relevant MOLECULE TYPE: peptide HYPOTHETICAL: NO ANTI-SENSE: NO FEATURE: LOCATION: 4..6 COTHER INPORMATION: OTHER INFORMATION: COTHER INFORMATION: COTHER INFORMATION: US-08-311-307B-4 CITY: HACKENSACK STATE: NEW JERSEY COUNTRY: U.S.A. OPERATING SYSTEM: 494 QCLQTLQG 501 5 QCLQTLQG 12 COUNTRY: U ZIP: 07601 σ RESULT ş ą /note: "The cysteine residues may be substituted with aminobutryic acid, homocysteine, or diaminosuberic acid." ö Gaps ö APPLICANT: Talmadge, James E. TITLE OF INVENTION: Polypeptide Agonist Derived From Human TITLE OF INVENTION: Interleukin-8 NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: 2 ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street CITY: Philadelphia Sequence 4, Application US/08311307B Patent No. 5627156 GENERAL INFORMATION: APPLICANT: Talmadge, James E. TITLE OF INVENTION: Polypeptide Agonist Derived From Human TITLE OF INVENTION: Interleukin-8 0; Indels Length 16; CUNTE: FA COUNTER: USA ZIP: 19103-2307 COMPUTER READABLE FORM: MEDIUM TYPE: FIAPPY disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE CONTWARE: PACADIL RECAMALES TO SOFFWARE: PACADIL RECAMALES OF ANDIA CURRENT APPLICATION DATA: B/11, 307B ATTICKENT NUMBER: US/08/311, 307B FILING DATE: 23-5EP-1994 ATTORNEY/AGENT NUMBER: US/08/311, 307B FILING DATE: 23-5EP-1994 ATTORNEY/AGENT NUMBER: 050085 TLING DATE: 23-569-1994 ATTORNEY/AGENT NUMBER: 630085 TELEPHONE: (215)563-4044 INFORMATION FRO TACT TELEPHONE: (215)563-4044 INFORMATION FOR 33: ELENCTH: 16 amino acids TRANDENESS. NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: Dann, Dorfman, Herrell and Skillman STREET: 1601 Market Street CITY: Philadelphia 1.4%; Score 8; DB 1; 100.0%; Pred. No. 0.91; tive 0; Mismatches COUNTRY: USA ZIE: 19103-2307 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPDY disk COMPUTER: IBM PC COMPATIble SS: not relevant not relevant NAME/KEY: Modified-site LOCATION: 4..6 Query Match 1.4 Best Local Similarity 100. Matches 8; Conservative CTHER INFORMATION: / CTHER INFORMATION: / CTHER INFORMATION: b CTHER INFORMATION: d US-08-311-3078-3 MOLECULE TYPE: peptide HYPOTHETICAL: NO 494 QCLQTLQG 501 5 0CLOTL0G 12 STRANDEDNESS: ANTI-SENSE: NO FEATURE: CITY: Phila STATE: PA STATE: PA TOPOLOGY : RESULT 8 US-08-311-307B-4 q 20

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COMPUTER: IBM PS/2 COMPUTER: NordPerfect 5.1 SOFTWARE: WordPerfect 5.1 SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/792,988 FILING DATE: 19911115 CLASSIFICATION 514 PRIOR APPLICATION NUMBER: 15/06 PRIOR APPLICATION NUMBER: ATTORNEY/AGENT INFORMATION: NAME: MONACON DATA: APPLICATION NUMBER: 30,480 RECEISTRATION NUMBER: 30,480 RECEISTRATION NUMBER: 30,480 RECEISTRATION NUMBER: 6066-159 TELEPAND CONDATION: TELEPANDEN (25)568-8383 TELEPANDEN (25)568-8383 TELEPANDEN (25)568-8383 TELEPANS: (215)568-8383 TELEPANS: (215)568-7583 TELEPANS: (215)568-7583 TELEPANS: (215)568-758	L.4%; Scol 20.0%; Pro 7e 0; h 5/07792988 5/07792988	TITLE OF INVENTION: CYTOPOIESIS by NUMBER OF SEQUENCES: 4 CORRESPONDENCE ADDRESS: ADDRESSEBE: University of Pennsylv STREET: Suite 419 STREET: 133 South 36th Street CITY: Philadelphia STRTE: Pennsylvania COUNTY: U.S.A. ZIP: 19104-3246	COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb COMPUTER: IBM PS/2 COMPUTER: IBM PS/2 SOFTWARE: NGOTOPErfect 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/792,988 FILING DATE: 19911115 CLASSIFICATION NUMBER: US/07/792,988 FILING DATE: 19911115 CLASSIFICATION NUMBER: US/07/792,988 FILING DATE: 19911115 CLASSIFICATION NUMBER: 05/07/792,988 FILING DATE: 19911115 CLASSIFICATION NUMBER: 05/07/792,988 FILING DATE: 19911115 CLASSIFICATION NUMBER: 05/07/792,988 FILING DATE: 19911115 CLASSIFICATION NUMBER: 05/07/792,988 FILING DATE: 0005005 FILING DATE: 000501115 TELEFAX: (215) 568-5549 TELEFAX: (215) 568-5549 TELEFAX: (215) 568-5549 TELEFAX: (215) 568-5549 TELEFAX: (215) 568-5549
APPLICATION NUMBER: US 08/105,105FILIGG DATE: 10-AUG-1993FILIGG DATE: 10-AUG-1993PRIOR APPLICATION NAMAR:APPLICATION NUMBER: US 07/914,045FILING DATE: 13-JUL-1995PRIOR APPLICATION NUMBER: US 07/914,045FILING DATE: 13-JUL-1995PRIOR APPLICATION NUMBER: US 07/399,971FILING DATE: 01-SEP-1989PRIOR APPLICATION NUMBER: US 07/240,078PRIOR APPLICATION NUMBER: US 07/240,078PRIOR APPLICATION NUMBER: US 07/240,078PRIOR APPLICATION NUMBER: US 07/240,078PRIOR APPLICATION NUMBER: US 07/104,827PRIOR APPLICATION NUMBER: US 06/766,852PRIOR APPLICATION NUMBER: US 06/144,098PRIOR APPLICATION NUMBER: US 06/144,098PILING DATE: 0-CCT-1987PRIOR APPLICATION NUMBER: US 06/144,098PRIOR APPLICATION NUMBER: US 06/144,098PILING DATE: 0-SEP-1983PRIOR APPLICATION NUMBER: US 06/144,098PILING DATE: 0-SEP-1981PRIOR APPLICATION NUMBER: US 06/756,952PRIOR APPLICATION NUMBER: US 06/756,952PRIOR APPLICATION NUMBER: US 06/756,952PRIOR APPLICATION NUMBER: US 06/756,952PRICATES OFFERE: 09-551,290PRILING DATE: 00-758-1981PRILING DATE: 00-759,932PRILING DATE: 00-759,932PRILING DATE: 00-759,932PRILING DATE: 00-759,932	O F. BURHARDO	Query Match1.4%;Score 8;DB 3;Length 37;Best Local Similarity100.0%;Pred. No. 1.9;Matches0;Gaps0;Matches8;Conservative0;Mismatches0;Indels0;0;Qy494OCLOTLOG 50111	RESULT 10 US-07-792-980-3 Sequence 3, Application US/07792988 Pattent NO. 5306709 GENERAL INFORMATION: APPLICANT: Gewirtz, Alan M. APPLICANT: Gewirtz, Alan M. TITLE OF INVENTION: Cytopoiesis by macrophage inflammatory proteins UNMBER OF SEQUENCES: NUMBER OF SEQUENCES: ADDRESSEE: University of Pennsylvania STREET: 133 South 36th Street CITY: Philadelphia STREET: 133 South 36th Street CITY: Philadelphia STREET: 133 South 36th Street CITY: Philadelphia STREET: 19104-3246 CONVTRY: U.S.A. MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

GENERAL INFORMATION:

FOR SEQ ID NO: 4: HARACTERISTICS: 73 amino acids WHNO ACID NESS: single stranded : linear	<pre>1 1.4%; Score 8; DB 1; Length 73; ' Similarity 100.0%; Pred. No. 3.5; 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 0/LOG 501 1111 0/PUCC 17</pre>	<pre>SBLT 12 :07-778 413E-19 Sequence 18, Application US/07778413E Sequence 18, Application US/07778413E Sequence 18, Application US/07778413E Sequence 18, Applications ENERRAL INFORMATION: A CLIVATION: A CLIVATION A CLIVATION: A CLIVATION A CLIVATI</pre>	1.4%; Score 8; DB 1; Length 73; milarity 100.0%; Pred. No. 3.5; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 106 501 111 106 17	13E-19 19, Application US/07778413E 0. 5401651
<pre>&gt; INFORMATION FOR SEQ ID NO &gt;&gt; SEQUENCE CHARACTERISTIC &gt;&gt; LENGTH: 73 amino aci TYPE: AMINO ACID &gt;&gt; TYPE: AMINO ACID &gt;&gt; TY</pre>	Query Match Best Local Similarity Matches 8; Conserv Qy 494 QCLQTLQG 501 11111111111111111111111111111111111	RESULT 12 US-07-778-413E-18 US-07-778-413E-18 Sequence 18, Application US/07 Patent No. 5401651 RESULTANT: Walz, Alfred TTTLE OF INVENTION: No. 54 TTTLE OF INVENTION: No. 54 CONRERSPONDENCE ADDRESS: 22 CORRESPONDENCE ADDRESS: 22 CORRESPONDENCE ADGRESS: 22 CORRESPONDENCE ADGRESS: 22 CORRESPONDENCE ADGRESS: 22 CORRESPONDENCE ADGRESS: 22 CONTRY: Thousand Oaks STREET: Angen Center STREET: Angen Center STREET: Agend Oaks CITY: Thousand Oaks STATE: California COUNTRY: USA CONPUTER READABLE FORM: MACINER STREET ANGEN CONPUTER READABLE FORM: MACINER STREET ANGEN APPLICATION STREE	Query Match Best Local Similarity Matches 8; Conserv Qy 494 QCLQTLQG 501 1111111 Db 10 QCLQTLQG 17	RESULT 13 US-07-778-413E-19 ; Sequence 19, Applicati ; Patent No. 5401651

GENERAL INFORMATION: GENERAL INFORMATION: ACTIVATING FACTORE TITLE OF INVENTION: ACTIVATING FACTORS TITLE OF INVENTION: ACTIVATING FACTORS CORRESSONDENCE ADDRESS: CORRESSONDENCE ADDRESS: ADDRESSEE: Amgen Inc. STREET: Amgen Center STREET: AMGEN COOK PATING STREET ATTON NUMBER: ASJ04 TELERAN: (805) 499-5725 EXTENSION 4955 TELERAN: (805) 499-5725 EXTENSION 4955 TREERERCE CHARACTERISTICS: LINFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 73 anino acids TELENTON FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LINFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 73 anino acids TELERAN: 11 near ; MOLECULE TYPE: peptide US-07-778-413E-19

ö Gaps ö 0; Indels Length 73; Query Match 1.4%; Score 8; DB 1; Best Local Similarity 100.0%; Pred. No. 3.5; Matches 8; Conservative 0; Mismatches 494 QCLQTLQG 501 10 QCLQTLQG 17 q δ

KESUUT 14 US-07-778-413E-20 Sequence 20, Application US/07778413E Patent No. 5401651 Releart No. 5401651 RERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Walz, Alfred TITLE OF INVENTION: No. 5401651el Neutrophil TITLE OF INVENTION: Activating Factors NUMBER OF SEQUENCES: 22 CORRESPONDENCE ADDRESS: ADDRESSEE: Angen Inc. STREET: Amgen Center STREET: Amgen Center STREET: Angen Center STREET: Angen Canter STREET: Angen Canter STREET: Angen Canter STREET: Angen Canter STREET: 19130-1789 COUNTRY: Thousand Oaks STATE: California COUNTRY: USA MEDIUM TYPE: DIskette, 3.5 in., DS, 2.0 MB MEDIUM TYPE: DIskette, 3.5 in., DS, 2.0 MB COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh OS 7.0 SOFTWARE: Microsoft Word Version 5.1a CURRENT APPLICATION DATA: APPLICATION NUMBER: US/07/778,413E FILING DATE: 16-0CT-1991 CLASSIFICATION: 536 RESULT 14

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; ATTORNEY/AGENT INFORMATION: ; NAME: Cook, Robert R. ; REGISTRATION NUMBER: 31602	Db 10 0CLOTLOG 17
REFERENCE/DOCKT NUMBER: A-204 TELECOMMUNICATION INFORMATION: TELEPHONE: (805) 499-5725 EXTENSION 4955 TELEFAX: (805) 499-5725 EXTENSION 4955 TELEFAX: (805) 499-9010: INFORMATION FOR SEQ ID NO: 20:	Search completed: September 25, 2001, 14:45:58 Job time: 138 sec
<pre>; SEQUENCE CHARACTERISTICS: ; LENGTH: 73 amino acids ; TYPE: amino acid ; TOPOLOGY: linear ; MOLECULE TYPE: peptide US-07-778-413E-20</pre>	
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CURRESSET: ANGEN TIC. STREET: ANGEN TIC. STREET: ANGEN Center STREET: 1840 Dehavilland Drive	
CONTRY INCUSATIO CAKS STATE: California CONTRY: USA ZIP: 91320-1789	
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) UPERATING STSTEM: MS-DOS 6.22 ) SOFTWARE: Microsoft Word Version 5.1a for ) USRENWT APPLICATION DATA	
ALTORNEL/AGENT INFORMATION: NAME: COCK RODERT R. REGISTRATION NUMBER: 31602 REFERENCE/DOCKET NUMBER: A-204A	
SEQUENCE CHARACTERISTICS: LENGTH: 73 amino acids TYPE: amino acid	
; TOPOLOGY: LINEAR ; MOLECULE TYPE: peptide US-08-340-102-18	
Query Match 1.4%; Score 8; DB 1; Length 73; Best Local Similarity 100.0%; Pred. No. 3.5;	
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hypothetical prote hypothetical prote beta 1,4 glucosylt hypothetical prote urracil DNA glycosy hypothetical prote protein T16B5,4 [ probable membrane 0-methyltranaferas probable GTP-bindi probable GTP-bindi probable GTP-bindi probable GTP-bindi probable GTP-bindi probable GTP-bindi	gans #text_change 15-Oct-1999 J GSPDB:GN00023; CESP:F55B12.3	Length 579; ; Indels 0; Gaps 0;	#text_change 04-Feb-2000 huber, J.; Wiemann, S. 2000 G0511	jth 524; Indels 0; Gaps 0;
<pre>2 T21359 2 A96532 2 B70450 2 B70450 2 S55641 2 S55641 2 H876063 1 2 H872063 2 T43215 2 T43215 2 T43215 2 T43215 2 A70340 2 A70340 2 A70340 1 RGB0B2</pre>	ALIGNMENTS - Caenorhabditis ele gans _revision 15-Oct-1999 brary, September 1996 brary, September 1996 ated from GB/EMBL/DDB ated from GB/EMBL/DDB ated from CB/EMBL/DDB ated from CB/EMBL/DDB	0%; Score 12; DB 2; .0%; Pred. No. 0.00071 .0; Mismatches 0	G0511.1 - human _revision 04-Feb-2000 .; Mewes, H.W.; Gassen ence Database, January ence Database, January ence stabase, January ence stabase, January fastis; clone DKFZp434	1.5%; Score 9; DB 2; Length 100.0%; Pred. No. 0.91; :ive 0; Mismatches 0; In
30 31 32 33 33 34 35 35 35 33 35 33 35 33 35 33 35 33 35 33 35 33 35 33 35 33 45 45 45 45 45 45 45 45 45 45 45 45 45	RESULT 1 T22703 hypothetical protein F55B12.3 C;Species: Caenorphabditis ele C;Species: T5-Oct-1999 #sequence C;Accession: T22703 R;Sims, M. A;Recession: T22703 A;Recession: T22703 A;Status: preliminary; transl A;Status: preliminary; transl A;Sta	Query Match 2. Best Local Similarity 100 Matches 12; Conservative QY 438 SGSLDTSIRVWD 449 Db 427 SGSLDTSIRVWD 438	RESULT 2 146310 hypothetical protein DKF2p434G0511 C;Species: Homo sapiens (man) C;Species: Homo sapiens (man) C;Date: 04-Feb-2000 %sequence_revi C;Accession: 146310 R;Duesterhoeft, A.; Lauber, J.; Me submitted to the protein Sequence submitted to the protein Sequence A;Reference number: 223035 A;Accession: 146310 A;Status: preliminary A;Status: preliminary A;Note: DKFZp434G0511.1	Query Match 1 Best Local Similarity 10 Matches 9; Conservativ

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A; Molecule type: protein A; Residues: 35-42, YY, 44, YX, 46-48 <SCH> A; Experimental source: dermal fibroblasts R; Golds, E.E.; Mason, P.; Nyirkos, P. Biochem. J. 259, 585-588, 1989 A; Title: Inflammatory cytokines induce synthesis and secretion of gro protein and a n A; Reference number: S03975; MUID:89246368 A; Accession: S03976 melanoma growth-stimulatory activity precursor - human N;Alternate names: fibroblast-derived neutroph11-activating protein gamma; GRO-alpha; C;Species: Homo sapians (man) C;Date: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 20-Aug-1999 C;Dates: 30-Jun-1989 #sequence\_revision 30-Jun-1989 #text\_change 20-Aug-1999 C;Accession: S13669; A28441; S00983; B60401; S03976; A47626; B46519 R;Baker, N.E.; Kucera, G.; Richmond, A. Nucleic Acids Res. 18, 6453, 1990 A;Title: Nucleotide sequence of the human melanoma growth stimulatory activity (MGSA) A;Reference number: S13669; MUID:91057157 A; Molecule type: MRNA A; Residues: 1-107 <RIC> A; Residues: 1-107 <RIC> A; Cross-references: EMBL:X12510; NID:934621; PIDN:CAA31027.1; PID:934622 A; Cross-references: ExbL:X12510; M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E S; Schroeder, J.M.; Sticherling, M.; Henneicke, H.H.; Preissner, W.C.; Christophers, E J. Immunol. 144, 2233-2232, 1990 A; Title: IL-lalpha or tumor necrosis factor-alpha stimulate release of three NAP-1/IL A; Reference number: A60401; MUID:90187866 A; Molecule type: protein A; Residues: 35-41, 'X', 43-49, 'X', 51-52, 'XX', 55-57 <GOL> A; Storroeder, J.M.; Persoon, N.L.M.; Christophers, E. J. Exp. Med. 171, 1091-1100, 1990 A; Title: Lipopolysaccharide-stimulated human monocytes secrete, apart from neutrophil ntity with melanoma growth stimulatory activity. A; Reference number: A47626; MUID:90217938 A; Accession: A47626 A;Reference number: A46519; MUID:93139489 A;Accession: B46519 RiAnisowicz, A.; Bardwell, L.; Sager, R. Proc. Natl. Acad. Sci. U.S.A. 84, 7188-7192, 1987 A.Title: Constitutive overexpression of a growth-regulated gene in transformed Chines A.Reference number: A94184; MUID:88041072 R;Richmond, A.; Baleitien, E.; Thomas, H.G.; Flaggs, G.; Barton, D.E.; Spiess, J.; Bo EMBO J. 7, 2025-2033, 1988 A;Title: Molecular characterization and chromosomal mapping of melanoma growth stimul A;Reference number: S00983; MUID:88328991 R; Proost, P.; De Wolf-Peeters, C.; Conings, R.; Opdenakker, G.; Billiau, A.; Van Damm J. Immunol. 150, 1000-1010, 1993 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-107 <BAK> A;Cross-references: EMBL:X54489; NID:934625; PIDN:CAA38361.1; PID:934626 A;Molecule type: mRNA A;Residues: 1-107 <ANI> A;Cross-references: GB:J03561; NID:9183622; PIDN:AAA35933.1; PID:9306806 A;Molecule type: protein A;Residues: 35-63,'X',65 <SC2> A;Experimental source: LPS-stimulated monocytes cells A;Cross-references: GDB:120181; OMIM:155730 A; Experimental source: MG-63 osteosarcoma A;Map position: 4q21-4q21 protein A;Molecule type: protei A;Residues: 35-62 <PRO> 494 QCLQTLQG 501 44 QCLQTLQG 51 A; Accession: A28414 A; Accession: S00983 A;Accession: B60401 A;Gene: GDB:GR01 ഗ C:Genetics

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C;Superfamily: beta-thromboglobulin F;1-34/Domain: signal sequence #status predicted <sig> F;35-107/Product: melanoma growth-stimulatory activity #status experimental <wat></wat></sig>	C;Accession: H70335 R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Vatire 302 353-358 1008
Query Match 1.4%; Score 8; DB 2; Length 107; Best Local Similarity 100.0%; Pred. No. 2.5; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus. A;Reference number: A70300; MUID:98196666 A;Recession: H70335 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
QY 494 QCLQTLQG 501 11111111 Db 44 QCLQTLQG 51	NID:92983063; PIDN:AAC06680.1; PID:9298
RESULT 6	A;Gene: ac.: A;Gene: ac.: C;Superfamily: Aquifex aeolicus hypothetical protein aq_397
<pre>crossed macrophage inflammatory protein 2 alpha precursor - human Macrophage inflammatory protein 2 alpha precursor - human N;Alternate names: gro-beta; growth regulated protein beta; melanoma growth-stimulatory C:Species: Homo sapiens (man) C:Species: Homos - 1991 #sequence_revision 30-Sep-1991 #text_change 20-Aug-1999 C:Accession: HDD31: A35031: A35030: A660075</pre>	Query Match 1.4%; Score 8; DB 2; Length 272; Best Local Similarity 100.0%; Pred. No. 5.7; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Rifekamp-Olson, P.; Gallegos, C.; Bauer, D.; McClain, J.; Sherry, B.; Fabre, M.; van Dev J. Exp. Med. 172, 911-919, 1990 A:Title: Cloning and characterization of CDNAS for murine macrophage inflammatory protei A:Reference number: J90200; MULD:90334732	OY         407         VWDPETET         414           11111111         1111111         111111         1111111           Db         161         VWDPETET         168
A:Accession: JH0281 A:Molecule type: mRNA A:Residues: 1-107 <tek></tek>	RESULT 8 S27707
A;CTOSS-TETERETENCES: GB:X537/99; NID:g34658; PIDN:CAA37808.1; PID:g34659 R;Lida, N.; Grotendorst, G.R. Mol. Cell. Biol. 10, 5596-5599, 1990 A;Title: Cloning and sequencing of a new gro transcript from activated human monovytes.	<pre>daunorubicin resistance protein - Streptomyces peucetius C;Species: Streptomyces peucetius C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 02-Feb-2001 C:Accession c:27207</pre>
A;Reference number: A35931; MUID:90377259 A;Accession: A35931 A;Molecule type: mRNA	Craccession: 22/10/ R;Guilfolie, P.G.; Hutchinson, C.R. submitted to the EMBL Data Library, August 1991 A;Description: A bacterial analog of the mdr gene of mammalian tumor cells is present
A; Kesslues; 1-10, ALIDS A;Crossreferences: GB:M57731; GB:M36964; NID;g183626; PIDN:AAA63182.1; PID;g183627 R;Haskill, S.; Peace, A.; Morris, J.; Sporn, S.A.; Anisowicz, A.; Lee, S.W.; Smith, T.; Proc. Natl. Acad. Sci. U.S.A.: 87, 7732-7736; 1990 A:Title: Identification of three related human CDO conse encoding nuclein function	
A; Reference number: A38290; MUID:91017578 A: Accession: A38290 A: Molecule type: mRNA	A;CLUSSTELETENCES: EMBL:M/3/30; NIU:GI33226; FLUN:AAA/4/1/.1; FID:GL33230 C;Genetics: A;Gene: drrA A;Start codon: GTG
A;Residues: 1-107 <has> A;Cross-references: GB:M3620; NID:g183628; PIDN:AAA63183.1; PID:g183629 A;Cross-references: GB:M3620; NID:g183628; PIDN:AAA63183.1; PID:g183629 T:Immunol. 144, 4434-4441, 1990 J. Titule: Monocyte adherence results in selective induction of novel mense sharing homola</has>	C;Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homolog C;Keywords: antibiotic resistance; ATP; nucleotide binding; P-loop F;24-215/Domain: ATP-binding cassette homology <abc> F;41-48/Region: nucleotide-binding motif A (P-loop)</abc>
A:Reference number: A60407; MUID:90257367 A:Accession: A60407 A:Status: not compared with conceptual translation A:Molecule type: mRNA	Query Match 1.4%; Score 8; DB 2; Length 330; Best Local Similarity 100.0%; Pred. No. 6.7; Matches 8: Conservative 0: Maismatches 0: Indels 0: Gaps 0:
A;Residues: 56-107 <spd> C;Superfamily: beta-thromboglobulin C;Keywords: inflammation F;1-34/Domain: signal sequence #status predicted <sig> F;35-107/Product: macrophage inflammatory protein 2 alpha #status predicted <mat></mat></sig></spd>	FSLG 66 1111 FSLG 299
Query Match 1.4%; Score 8; DB 2; Length 107; Best Local Similarity 100.0%; Pred. No. 2.5; Matches 0; Gaps 0; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	RESULT 9 T27762 hypothetical protein ZK177.6 - Caenorhabditis elegans C:Species: Caenorhabditis elegans C:DFF-:15-:Cort-1000 #econord action 15-Cort-1000 #econord
0y 494 OCLOTLOG 501 11111111 Db 44 QCLOTLOG 51	oct 1995 *teat_cumuye 19 oct 1995 1995 cosmid 2K177.
RESULT 7 H70335 hypothetical protein ag_397 - Aquifex aeolicus C:Species: Aquifex aeolicus C:Species: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Nov-1999	A;Reference number: 220416 A;Accession: T27762 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Nolecule type: DNA A;Residues: 1-336 <and> A;Cross-references: EMBL:U21321; PIDN:AAB36970.1; GSPDB:GN00020; CESP:ZK177.6</and>

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A:Experimental source: strain Bristol N2; clone ZK177 C;Genetics: A;Gene: CESP:ZK177.6 A:Map position: 2 A:Introns: 44/1; 75/3; 103/1; 185/3; 283/1	RESULT 12 A43289 CDC4L protein - human (fragment) N;Alternate names: cell division control protein CDC4 homolog C;Species: Homo sapiens (man)
Query Match 1.4%; Score 8; DB 2; Length 336; Best Local Similarity 100.0%; Pred. No. 6.9; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	C;Date: 27-Apr-1993 #sequence_revision 26-Jul-1996 #text_change 15-Aug-1997 C;Accession: A43289; S30330 R;Feuchter, A.E.; Freeman, J.D.; Mager, D.L. Genomics 13, 1237-1246, 1992
QY 525 DGTVKLWD 532 11111111 Db 219 DGTVKLWD 226	A;Tille: Stategy for detecting certural transcripts promoted by numan endogenous ton A;Reference number: A43289; MUID:92372019 A;Accession: A43289 A;Molecule type: mRNA A;Residues: 1-515 <feu></feu>
RESULT 10 145774 odorant receptor 1 - channel catfish C:Species: Ictalurus punctatus (channel catfish) C:Date: Io:Peb-1995 #sequence_revision 20-Feb-1995 #text_change 04-Sep-1998 C.Accession: T45774	A;Cross-references: EMBL:M83822 A;Note: sequence extracted from NCBI backbone (NCBIP:111997) C;Genetics: A;Gene: GDB:CDC4L A;Cross-references: GDB:131404 A;Map position: 19p13.3-19p13.3
Ringal, J.; Dowling, M.M.; Buck, L.; Axel, R.; Chess, A. Cell 72, 657-666, 1993 A:Title: The family of genes encoding odorant receptors in the channel catfish. A:Reference number: A45774; MUID:93201590	Query Match 1.4%; Score 8; DB 2; Length 515; Best Local Similarity 100.0%; Pred. No. 10; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A:/Status: preliminary; not compared with conceptual translation A:Molecule type: mRNA A:Residues: 1-344 <nga></nga>	QY 358 SGSRDATL 365 11111111 DD 482 SGSRDATL 489
A;Experimental source: olfactory epithelium A;Note: sequence extracted from NCBI backbone (NCBIP:127744) C;Superfamily: olfactory receptor OR14 C;Keywords: olfaction; transmembrane protein	RESULT 13 T16607 hvootbeitcal nrotein K1082 1 - Caenorhahditis elegans
Query Match 1.4%; Score 8; DB 2; Length 344; Best Local Similarity 100.0%; Pred. No. 7; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999 C;Accession: T16607 R;Miller, N.
QY 33 IFSISIIA 40 11111111 DD 157 IFSISIIA 164	submitted to the EMBL Data Library, June 1995 A;Description: The sequence of C. elegans cosmid K10B2. A;Reference number: 218545 A;Accession: T16607 A;Status: preliminary; translated from GB/EMBL/DDBJ
RESULT 11 T26805 hypothetical protein Y41C4A.11 - Caenorhabditis elegans C.Species: Caenorhabditis elegans C.Species: Coenorhabditis elegans C.Accession: T26805	A; Molecule type: DNA
Risteward, C. submitted to the EMBL Data Library, October 1998 ArReference number: 220269 ArAccession: T26805 ArStetus: preliminary; translated from GB/EMBL/DDBJ	Query Match 1.4%; Score 8; DB 2; Length 701; Best Local Similarity 100.0%; Pred. No. 13; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
A; Residues: 1-36. CMLL A; Residues: 1-36. CMLL A; Cross-references: EMBL:AL032627; PIDN:CAA21549.1; CESP:Y41C4A.11 A; Experimental source: clone Y41C4A C; Genetics:	QY 446 RVMDVETG 453 111111111 DD 321 RVWDVETG 328
A;Gene: CESP:Y41C4A.11 A;Introns: 24/3; 40/3; 100/1; 146/3; 306/3; 350/2	RESULT 14 A86243 Hunseltan several (imposted) - Arabidonsis thaliana
Query Match Best Local Simila Matches 8; Co	nypounerical procent inmported 7 analyzopara unaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C;Accession: A6543 R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
QY 275 RIVSGSDD 282          Db 290 RIVSGSDD 297	Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000 A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

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C.A.: Li, J.H.: Li, Y.: Lin, X.: Liu, S.X.: Liu, Z.A.: Luros, J.S.: Maiti, R.: Marziali, Rizzo, M.: Rooney, T.: Rowley, D.: Sakano, H. A.Authors: Salzberg, S.L.: Schwartz, J.R.: Shinn, P.: Southwick, A.M.: Sun, H.: Tallon, Ker, M.; Wu, D.: Yu, G.: Fraser, C.M.: Venter, J.C.: Davis, R.W. A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A:Reference number: A86141; MUID:21016719 A:Reference number: A86141; MUID:21016719 A:Residues: Preliminary A:Relevence in Part A:Residues: 1-821 <STOS A:Residues: 1-82 capbid protein - Leishmania RNA virus 2 (fragment) c.Species: Leishmania RNA virus 2 C:Species: Leishmania RNA virus 2 C:Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 18-Jul-1997 C:Accession: 556768 R:Widmer, G.; Dooley, S. Nucleic Acids Res. 23, 2300-2304, 1995 A;Title: Phylogenetic analysis of Leishmania RNA virus and Leishmania suggests ancient v A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania suggests ancient v A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania suggests ancient v A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania suggests ancient v A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania suggests ancient v A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania suggests ancient v A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania suggests ancient v A;Reston: S56768 A;Accession: S56768 A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania suggests ancient v A;Reston: S56768 A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania suggests ancient v A;Reston: S56768 A;Cossion: S56768 A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania Suggests ancient v A;Reston: S56768 A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania Suggests ancient v A;Reston: S56768 A;Cossion: S56768 A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania Suggests ancient v A;Reston: S56768 A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania Suggests ancient v A;Reston: S56768 A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania Suggests ancient v A;Reston: S56768 A;Ritle: Phylogenetic analysis of Leishmania RNA virus and Leishmania RNA virus ö ö Gaps Gaps ö ö Query Match1:4%;Score 8;DB 2;Length 821;Best Local Similarity100.0%;Pred. No. 15;Matches8;Conservative0;Mismatches0; 0; Indels Length 40; Query Match 1.2%; Score 7; DB 2; Best Local Similarity 100.0%; Pred. No. 12; Matches 7; Conservative 0; Mismatches Search completed: September 25, 2001, 14:46:28 Job time: 138 sec 520 ITSSDDGT 527 426 ITSSDDGT 433 393 GRRVVSG 399 11 GRRVVSG 17 15 RESULT S56768 γ q δ q

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<pre>RN [1] RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. RA Schwartz D., Chaverri-Alamada L., Berliner J., Kirchgessner T., RA Quisomoro D., Fang J., Tekamp-Olson P., Lusis J., Fogelman A., RA Territo M.; RL Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases. CC -i- FUNCTION: PLAYS A ROLE IN MONOCYTE ADHESION TO THE ENDOTHELIUM. CC -i- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE CC -i- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE CC -i- SIMILARITY: EXEONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE CC -i- SUMILARITY: EXEONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE CC -i- SIMILARITY: EXEONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE)</pre>	CC This SWISS-PROT entry is copyright. It is produced through a collaboration cC This SWISS-PROT entry is copyright. It is produced through a collaboration cC between the Swiss Institute of Buloinformatics and the EMBL dutstation - cC the European Bloinformatics Institute. There are no restrictions on its cC use by non-profit institutions as long as its content is in no way cC modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ cC resentities requires alicense(isb-sib.ch). CC resentities requires alicense(isb-sib.ch). DR RESP: projati JMGS. DR RESP: projati JMGS. D	Mat	RESULT 4 GROA_BOVIN STANDARD; PRT; 104 AA. GROA_BOVIN STANDARD; PRT; 104 AA. AC 046676; DT 15-DEC-1998 (Rel. 37, Created) DT 15-DEC-1998 (Rel. 37, Last sequence update) DT 15-DEC-1998 (Rel. 37, Last annotation update) DT 15-DEC-1998 (Rel. 37, Last annotation update) DT 15-DEC-1998 (Rel. 37, Last annotation update) DT 15-DEC-1998 (Rel. 37, Last sequence update) DT 15-DEC-1998 (Rel. 37, Rel. 3	<pre>RN [1] RP SEQUENCE FROM N.A. YOShIMURA T., Modi W.S.; RL SUBMITTED (MAR-1997) to the EMBL/GenBank/DDBJ databases. SUBMITTED (MAR-1997) to the EMBL/GenBank/DDBJ databases. CC</pre>
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Db 41 QCLQTLQG 48	SUL			<pre>KW I'J RP SEQUENCE FROM N.A. RX MEDLINE-88328991; PubMed-2970963; RA Richmond A., Balentien E., Thomas H.G., Flaggs G., Barton D.E., RA Spiess J., Bordoni R., Francke U., Derynck R.; RT "Molecular characterization and chromosomal mapping of melanoma RT growth stimularory activity, a growth factor structurally related to RL EMBO J. 7:2025-2033(1988). RU 53</pre>	<pre>RP SEQUENCE OF 35-65. RX MEDLINE=90219395; Pubmed=2182761; RA Schroeder JM., Persoon N.L.M., Christophers E.; RA Schroeder JM., Persoon N.L.M., Christophers E.; RT "Lipopolysaccharide-stimulated human monocytes secrete, apart from RT neutrophil-activating peptide 1/interleukin 8, a second neutrophil- RT activating protein. NH2-terminal amino acid sequence identity with RT melanoma growth stimulatory activity."; RL J. Exp. Med. 171:1091-1100(1990).</pre>	 	RP STRUCTURE BY NMR. RP STRUCTURE BY NMR. RX MEDLINE-93387459; PubMed-8397104; RA Fairbrother W.J., Reilly D., Colby T., Horuk R.; RT "IH assignment and secondary structure determination of human RT melanoma growth stimulating activity (MGSA) by NMR spectroscopy."; RL FEBS Lett. 330:302-306(1993).
	DR Pfam; FF00048; ILB; IL DR PRINTS; PR00436; INTERLEUKINB. DR PRINTS; PR00436; INTERLEUKINB. DR PROSTTE; PR00471; SMALLCYTOKINES_CXC; 1. KW CYtokine; Growth factor; Inflammatory response; Signal. FT SIGNL 1 30 POTENTIAL. FT CHAIN 31 104 GROWTTAL. FT CHAIN 31 104 GROWTTAL. FT DISULFID 42 82 BY SIMILARITY. FT DISULFID 42 82 BY SIMILARITY. FT DISULFID 42 82 BY SIMILARITY.	Query Match Best Local Simil Matches 8; C	QY 494 OCLOTLOG 501 Db 41 QCLOTLOG 48 RESULT 5 GROB BOVIN		CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC The European Bioinformatics Institute of Bioinformatics and the EWBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its CC use by non-profit institutions as long as its content is in no way CC entities requires a license agreement is not removed. Use by and for commercial CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ CC or send an email to license@isb-sib.ch).		Query Match 1.4%; Score 8; DB 1; Length 104; Best Local Similarity 100.0%; Pred. No. 1.4; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 494 QCLQTLQG 501

<pre>OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. OX NCBI_TaxID=9606; RN [1] RN [1] RN [1] RN [1] RN [1] RN [1] RN PEQUECE FROM N.A. RC TISSUS-HISTLOCYTIC LYMPhoma; RX MEDLINE=90354792; PubMed=2201751; RA MEDLINE=90354792; PubMed=2201751; RA PEQUECE FROM N.A. RX MEDLINE=90354792; PubMed=2201751; RA TESSUS-HISTLOCYTIC LYMPhoma; RX MEDLINE=90354792; PubMed=2201751; RA Fabre M., Van Deventer S., Cerami A.; RA Fabre M., Van Deventer S., Cerami A.; R1 T. Texpen Med. 172:911-919(1990). R1 J. Exp. Med. 172:911-919(1990).</pre>	SEQUENCE FROM N.A. MEDLINE-90377259; PubMed-20782 Iida N., Grotendorst G.R.; "Cloning and sequencing of a n monocytes: expression in leuko Mol. Cell. BJOL. 10:5596-5599( [3] SEQUENCE FROM N.A. MEDLINE-91017578; PubMed-22172 Haskill S., Peace A., Morris J Smith T., Martin G., Ralph P., "Identification of three relat functions.";	<pre>RL Proc. Natl. Acad. Sc1. U.S.A. 87:7732-7736(1990).</pre>	This the l the l use modi: or se		· ·
<pre>RN [8] RP STRUCTURE BY NMR. RP STRUCTURE BY NMR. RX MEDLINE-94376296; PubMed-8089846; RA Fairbrother W.J. Rellly D., Colby T., Hesselgesser J., Horuk R.; RT The solution structure of melanoma growth stimulating activity."; RL J. Mol. Blol. 242:252-270(1994). R1 J. Mol. Blol. 242:252-270(1994). R2 STRUCTURE BY NMR. R2 MEDLINE-95105175; PubMed-7806518; R4 MEDLINE-95105175; PubMed-7806518; R5 Kim K.S., Clark-Lewis I., Sykes B.D.; R5 Solution structure of GRO/melanoma growth stimulatory activity R1 J. Blol. Chem. 269:32909-32915(1994). R1 J. Blol. Chem. 269:32909-32915(1994).</pre>		CC	DR PROSITE: PS00471; SWALL_CYTOKINES_CXC; 1. KW Cytokine; Growth factor; Inflammatory response; Signal; 3D-structure. FT SIGNAL 1 34 FT CHAIN 35 107 FT DISULFID 43 69 FT DISULFID 45 85 FT DISULFID 45 85 FT DISULFID 45 11301 MW; 17048A6B4D765CA2 CRC64;	Query Match1.4%;Score 8;DB 1;Length 107;Best Local Similarity100.0%;Pred. No. 1.5;0;Indels0;Matches8;Conservative0;Mismatches0;Indels0;Qy494QCLOTLQG 5011111111Db44QCLOTLQG 51Db44QCLOTLQG 51	RESULT 7 MIZA_HUMAN STANDARD; PRT; 107 AA. ID MIZA_HUMAN STANDARD; PRT; 107 AA. AC P19875; 090PB8; DT 01-FEB-1991 (Rel. 17, Last sequence update) DT 01-0CT-2000 (Rel. 40, Last sequence update) DT 01-0CT-2000 (Rel. 40, Last annotation update) DE MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA PRECURSOR (MIP2-ALPHA) (GROWTH REGULATED PROTEIN BETA) (GRO-BETA). DE REGULATED PROTEIN BETA) (GRO-BETA). AM GROZ OR GROB OR MIPZA. OS HOMO Sapiens (Human).

FT DISULFID 45 85 BY SIMILARITY. FT CONFLICT 27 28 AA -> G (IN REF. 2). SQ SEQUENCE 107 AA; 11342 MW; 97A69946B7F1F070 CRC64; Query Match 1.4%; Score 8; DB 1; Length 107; Best Local Similarity 100.0%; Pred. No. 1.5; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 494 QCLQTLQG 501         DD 44 QCLQTLQG 51	RA_	CC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces. OX NCBI_TAXID=1950; Streptomycineae; Streptomycetaceae; Streptomyces. OX NCBI_TAXID=1950; Streptomycineae; Streptomycetaceae; Streptomyces. OX NCBI_TAXID=1950; Streptomyces. RP SEQUENCE FROM N.A. RP SECUENCE FROM N.A. RP S	R Procludicity Cade Sci. U.S.A. 88:8553-8557(1991). R Proc. Natl. Acad. Sci. U.S.A. 88:8553-8557(1991). CC -1- FUNCTION: DRRA AND DRRB MAY ACT JOINTLY TO CONFER DAUNORUBICIN AND CC DOXORUBICIN RESISTANCE BY AN EXPORT MECHANISM. CC -1- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT PROTEIN FAMILY CC (ABC TRANSPORTERS).	This SWISS-PROT entry is between the Swiss Institu- the Buropean Bioinformati- use by non-profit inst modified and this stateme- entities requires a licen.		<pre>FT NP_BIND 41 48 ATP (BY SIMILARITY) FT NP_BIND 41 48 ATP (BY SIMILARITY) SQ SEQUENCE 330 AA; 35700 MW; 582D66C90D54E6B9 CRC64; Query Match 1.4%; Score 8; DB 1; Length 330; Best Local Similarity 100.0%; Pred. No. 4; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0; OY 59 EVREFSIG 66</pre>	Db 292 EVRSFSLG 299 RESULT 10 YSS1_CABEL STANDARD; PRT; 701 AA. AC 009990; DT 15-JUL-1998 (Rel. 36, Created)
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<pre>RP SEQUENCE OF 1405-1918 FROM N.A. XX MEDLINE-92372019; PubMed~1505956; RA Feuchter A.E., Freeman J.D., Mager D.L.; RT "Strategy for detecting cellular transcripts promoted by human RT endogenous long terminal repeats.identification of a novel gene RT (CDC4L) with homology to yeast CDC4."; RL Genomics 13:1237-1246(1992). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS). CC -1: SIMILARITY: CONTAINS AT LEAST 2 WD REPEATS (TRP-ASP DOWAINS).</pre>		SS et A	SUL SS_		RT gene family."; RT gene family."; RL Plant Physiol: 96:77-83(1991). CC -1 FUNCTION: FEREDOXINS ARE IRON-SULEUR PROTEINS THAT TRANSFER CC -1 - COFACTON: BINDS A VARIETY OF METABOLIC REACTIONS. CC -1 - COFACTON: BINDS A ZFB-2S CLUSTER. CC -1 - SUBGELLULAR LOCATION: CHLOROPLAST. CC -1 - SUBGELLULAR LOCATION: CHLOROPLAST. CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC This SWISS-PROT entry is copyright. It is produced through a collaboration CC the European Bioinformatics Institute of Bioinformatics and the EMBL outstation CC use by non-profit institutions as long as its content is in no way
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sYLASE (EC 3.2.2.-) (UDG). 255 AA. 314 AA. U\_DNA\_GLYCOSYLASE; 1. PRT ; PRT ; -----13834.1; -. ANDARD; 043; -. NG; 1. ANDARD; e.

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.	OM protein – protein search, using sw model Run on: September 25, 2001, 14:45:36 ; Search time 22.42 Seconds (without alignments) 3475.810 Million cell updates/sec	Title: US-09-328-877A-8 Perfect score: 589 Sequence: 1 MSKPGKPTLNHGLVPVDLKSSRNGTEETKLLVLDFDVDMK 589	Scoring table: OLIGO Gapop 60.0 , Gapext 60.0	Searched: 425026 seqs, 132305027 residues	Word size : 0	Total number of hits satisfying chosen parameters: 425026	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Listing first 45 summaries	2: sp_bacceria:* 3: sp_tungi:* 4: sp_humar:*	ເບັດເບັ	<pre>10: sp_plant:* 11: sp_rodent:* 12: sp_unclassified:* 13: cp_vortebrasified:*</pre>	 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES		Score Match Ler	540 91.7 553 4 Q9NUX6 Q9nux6 21 3.6 1326 5 Q9V2F4 Q9vzf4	12 2.0 587 5 044083 10 1.7 310 4 075938	10 1.7 357 4 095320 055320 055320 homo	9 1.5 524 4 C	9 1.5 703 11 Q9WVM9 09 09WVM9 mus 9 1.5 741 4 Q9H9K3 09h9K3 homo	9 1.5 845 10 Q9LJR3 0 9 1.5 1028 4 Q9HCM8 00 09hcm8 hor	9 1.5 2904 11 09EPNO 9 1.5 2931 11 09EPM9	9 1.5 2936 11 Q9EPN1 Q9Epn1 m B 1.4 272 2 066716 006716 aq	17         8         1.4         2.6         5         97477         09477         094777           18         8         1.4         326         5         094072         094977         094977           18         8         1.4         326         5         094072         094977         094977           19         8         1.4         327         5         076523 </td

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<pre>RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Lu X., Watel B., McTntosh T.C., McCeod M.P., McPherson D., RA Liu X., Waltow G., Milshina N.V., McDarry C., Mortis J., Moshrefi A., RA Mount S.M., Noy M., Murphy B., Murphy L., Murry D.M., Nelson D.L., RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Balazzolo M.P. Hitman G.S., Pan S., Pollard J., Purl V., Reese M.G., RA Shue B.C., Siden-Kiamo S.I., Sanders R.D.C., Scheeler F., Shen H., Shere B.C., Stapleton M., Strong R., Sun E., Shere B.C., Stapleton M., Strong R., Shun F., RA Shier E., Spradinja A.C. Stapleton M., Stuong R., Shun F., RA Shier E., Spradinja A.C. Katpleton M., Stuong R., Shun F., RA Shier E., Spradinja A.C. Katpleton M., Stuong R., Shun F., RA Shier E., Spradinja A.C. Katpleton M., Stuong R., Shun F., RA Shier E., Spradinja A.C. Katpleton M., Stuong R., Shun F., RA Shier E., Spradinja A.C. Katpleton M., Stuong R., Shun F., RA Shier E., Stapleton M., Stuong R., Shun S., RA Hilliams S.M., Wooley T., Worley K.C., Wu D., Yang S., Yao O.A., RA Shens R.J. Venter J. S., Zhan M., Zhau S., Zhu X., Smith H.O., RA Shens Fagn0035516; CG15010. RE EL, Stonger M., Ruolay K.C., Wu D., Yang S., Yao O.A., RA Gibbs R.A., Neyer B.M., Nenter J.C.; RE Stence 287:2195(2000). RE BML; AE003409; AGC32461 RE FURMS; PF000640; F-Dox; 1. RE RE R.B. AE0035016; CG15010. RE RE R.B. AE0035016; CG15010. RE RE R.B. AE00320; Genore M., Stecors Ster. *; Repeat: MD F00646; F-Dox; 1. RE RE R. REPORTERRET RE RE RE REPARTES S. REPRETE PS00181; FB0X; 1. REPRETE PS00181; FB0X; 1. REPRETE PS0018; MD_REPARTE; S. KW Repeat: MD F00646; F-Dox; 1. Repeat: MD F00646; F-Dox; 1. REPRETE REPORTERRETE S. REPRETE REPORTERRETE S. REPRETE REPORTERRETE S. REPRETE REPORTERRETE S. REPRETE REPORTERRETE S. REPRETE REPORTERRETE S. REPRETE REPORTERRETE S. SEQUENCE 1326 AM: 141360 MM; 3F426973CFA3027F CKC4; SEQUENCE 1326 AM: 141360 MM; SF42673CFA3027F CKC4; SEQUENCE 1326 AM: 141360 MM; SF42673CFA3027F CKC4; SEQUENCE 1326 AM; 141360 MM; SF42673CFA3027F CKC4; SEQUEN</pre>	Aat Mat 408	C Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhadditidae; Peloderinae; Caenorhabditis. N [1] RP SEQUENCE FROM N.A. SEQUENCE FROM N.A. RA Hubbard E.J.A., Wu G., Kitejewski J., Greenwald I.; RA Hubbard E.J.A., Wu G., Kitejewski J., Greenwald I.; "sel-10, a negative regulator of lin-12 activity in Caenorhabditis RT elegans, encodes a member of the CDC4 family of proteins."; RE Genes Dev. 11:182-3193(1997). RI FIGHI, FROJORA12 DR InterPro; IPROOL680: - DR InterPro; IPROOL680: - DR InterPro; IPROOL680: - DR RICEPROS 1PROOL680: - DR RICEPROS 200405; WOLM - DR RICEPROS 200405; WOLM - RICEPROS 200405; REDEARS UNKNOW - SEQUENCE 587 AA; 65311 MW; 2D3700445; REDEARS 200545; RUKUMA - SEQUENCE 587 AA; 65311 MW; 2D3700445; REDEARS 200545; RUKUMA - SEQUENCE 587 AA; 65311 MW; 2D3700445; RUKUMA - RUKUMA - RU
<ul> <li>QY 110 VOPPTCLOEWLKMFOSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFORDFISLLPKE 169</li> <li>T4 VOPPTGLOEWLKMFOSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFORDFISLLPKE 133</li> <li>QY 170 LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGFI 229</li> <li>Di 134 LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGFI 193</li> <li>QY 230 HSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWS 289</li> <li>Di 194 HSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWS 253</li> <li>QY 230 AVTGKCLRTLVGHTGCWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCM 349</li> <li>Di 194 HSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWS 253</li> <li>QY 230 HSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWS 253</li> <li>QY 350 HLHERKVSSSRDATLAVMDIETGQCLHVLMGHVAAVRCVQYDGRRIVSGSADRTLKVWN 373</li> <li>QY 410 PETETCLHTLOGHTNRVSLOPGIHVVSGSLDTSIRVWDVETGOCIHTLYGHQSLTSGM 469</li> <li>Di 11111111111111111111111111111111111</li></ul>	SUL	<pre>K FXDINEBERKLEY; K FXDINEBERKLEY; K FXDINEBERKLEY; K MEDLINE-20196006; PubMed=10731132; K MEDLINE-20196006; PubMed=10731132; K Adams W.D. Cclanker S.E. VLI F.M., Hoskins R.A., Gacayne J.D., K Adams W.D. Cclanker S.E. VLI P.W., Hoskins R.A., Galle R.F., K George R.A. Lewis S.E. VLI P.W., Hoskins R.A., Galle R.F., K George R.A. Lewis S.E. VLI P.W., Hoskins R.A., Galle R.F., K George R.A. Lewis S.E., Nandell M.D., Zhang O., Chen L.X. K Adams W.E.C., Batzel R.G., Nelson C.R., Miklos G.L.G., K Adams K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Bandon R.C., Rogers Y.H.C., Blazel R.G., Champe M., Pfeiffer B.D., K Adan K.H., Boyle C., Baxter G., Baldwin D., Ballew R.M., Basu A., Batuek J., Bayraktaroglu L., Beasley E.M., R Berson K.Y., Benos P.V., Bouck J., Bayraktaroglu L., Beasley E.M., R Berson K.M., Bouck J., Burkstein P., Brottier S. R Berson K.M., Bouck J., Burkstein P., Brottier S., R Bertis K.C., Busam D.A., Bulle C., Mavenport L.B., Davies P., R Dodson K., Doup L.E., Downes M., Duger R., Dietz S.M., R Dodson K., Doup L.E., Downes M., Dugar Rocha S., Punkov B.C., Dunn P., R Dodson K., Dunp L.E., Downes M., Dugar Rocha S., Pielschmann W., R Stris N.L., Harvey D., Hennan T.J., Med MH., Ibegwan C., R Harris N.L., Harvey D., Hennan T.J., Wei MH., Ibegwan C., R Harris N.L., Harvey D., Howland T.J., Wei MH., Ibegwan C., R Harris N.L., Harvey D., Howland T.J., Wei MH., Ibegwan C., R Harris N.L., Harver S., Kulp D., Lai Z., K Hantis N., Harvei C., Kravitz S., Kulp D., Lai Z., K Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., K Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., K Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., K Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., K Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., K Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., K Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., K Hamel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D.,</pre>

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Gaps Gaps Homo sapiens (Human). Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia: Butheria; Primates; Catarrhini; Hominidae; Homo. NCBL\_TaxID=9606; Homo sapiens (Human). Eukaryota; Metazoa; Chudata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBL\_TaxID-9606; Tcherrev V.T., McMurtrie E.B., Nguyen Q.A., Mishra V.S., Barbosa M.D.F.S., McIndoe R., Kingsmore S.F.; "Identification of LYST2, a brain-specific member of the Chediak-Higashi syndrome gene family."; Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases, EMBL; AFO72371; AAD41633.1; -. InterPro; IPR001680; -. ö ö Query Match1.7%; Score 10; DB 4; Length 357;Best Local Similarity100.0%; Pred. No. 0.14;Matches10; Conservative0; Mismatches Length 472; 0; Indels 472 AA; 52810 MW; 679A710103FDAE5E CRC64; 357 AA; 39298 MW; 87A265539437BD86 CRC64; 01-0CT-2000 (TrEMBLrel. 15, Created) 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) 01-0CT-2001 (TrEMBLrel. 16, Last annotation update) HYPOTHETICAL 58.8 KDA PROTEIN. DKFZP434G0511. 01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last sequence update) 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) LYSOSOMAL TRAFFICKING REGULATOR 2 (FRAGMENT). InterPro; IPR002106; -. Pfam; PF00400; WD40; 7. PRINTS; PR00320; GROTEINBRPT. PROSTE; PS00339; AA\_TRNA\_LIGASE\_II\_2; UNKNOWN\_1. PROSTE; PS00678; WD-REPEATS; UNKNOWN\_5. SMART; SN00320; WD40; 1. SRPEAT; WD 10920; MD40; 1. SEQUENCE 357 AA; 39298 MM; 87A265539437BD86 C Ouery Match 1.5%; Score 9; DB 4; Best Local Similarity 100.0%; Pred. No. 2; Matches 9; Conservative 0; Mismatches 472 AA. 524 AA. PRT ; PRT; PROSITE; PS50197; BEACH; 1. SMART; SM00320; WD40; 1. **PRELIMINARY**; **PRELIMINARY**; Pfam; PF00400; WD40; 4. 523 SDDGTVKLWD 532 171 SDDGTVKLWD 180 357 VSGSRDATL 365 SEQUENCE FROM N.A. 313 VSGSRDATL 321 Repeat; WD repeat SEQUENCE NON\_TER (1USN90) Q9Y6J1 **LUSN60** Q9Y6J1 ە ~ Ξ RESULT RESULT Q9Y6J1 **USN90** qq Qλ SO DRAWN CONSTRUCTION CONSTRUCTICONSTRUCTICA CONSTRUCTICA οy q £ ö ö MEDLINE-98400255; Pubmed-9731529; MEDLINE-98400255; Pubmed-9731529; Neubauer G., King A., Rappsilber J., Calvio C., Watson M., Ajuh P., Sleeman J., Lamond A., Mann M.; Mass spectrometry and EST-database searching allows characterization of the multi-protein spliceosome complex."; Nat. Genet. 20:46-50(1998). EMBL; AF083333; AAC64084.1; -InterPro; IPR0021680; -InterPro; IPR0021680; -InterPro; PP002160; -Pfam; PF00400; WD40; 6. Gaps Gaps AEDLINE-99449965; PubMed-9774689; AEDLINE-99449965; PubMed-9774689; Achsel T., Ahrens K., Brahms H., Teigelkamp S., Luhrmann R.; "The human U5-220kD protein (hPrp8) forms a stable RNA-free complex with several U5-specific proteins, including an RNA unwindase, a homologue of ribosomal elongation factor EF-2, and a novel WD-40 Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. UO SNAME STATUTE Homo Sapiens (Human). Eukaryota: Metazoa; Chantata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. ö ö 2.0%; Score 12; DB 5; Length 587; 100.0%; Pred. No. 0.0019; Live 0; Mismatches 0; Indels 1.7%; Score 10; DB 4; Length 310; 100.0%; Pred. No. 0.13; Indels 310 AA; 34290 MW; 7347F144E7D9796E CRC64; 01-MAY-1999 (TTEMBLrel. 10, Created) 01-MAY-1999 (TTEMBLrel. 10, Last sequence update) 01-MAR-2001 (TTEMBLrel. 16, Last annotation update) 01-MAR-SPECIFIC 40 KDA PROTEIN. ö PRINTS; PRO0320; GPROTEINBRPT. PROSTTE; PRO0339; AA\_TRNA\_LIGASE\_II\_2; UNKNOWN\_1. PROSTTE; PS00319; WD\_REPEATS; UNKNOWN\_5. SWART; SM00320; WD40; 1. Repeat. WD repeat. 310 AA. 357 AA. Query Match1.7%; Score 10; DBBest Local Similarity100.0%; Pred. No. 0.1Matches10; Conservative0; Mismatches protein."; Mol. Cell. Biol. 18:6756-6766(1998). EMBL; AF090988; AAC69625.1; -. InterPro; IPR001680; -. PRT ; PRT ; Best Local Similarity 100. Matches 12; Conservative **PRELIMINARY**; · PRELIMINARY; 438 SGSLDTSIRVWD 449 435 SGSLDTSIRVWD 446 523 SDDGTVKLWD 532 112 SDDGTVKLWD 121 SEQUENCE FROM N.A. SEQUENCE FROM N.A. NCBI\_TaxID=9606; Query Match SEQUENCE 075938; 075938; 095320; 095320 4 ŝ Ξ RESULT 075938 δ q SOW SOULD STRUCT S q ş

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Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBL_TaxTD=9606; [1] [1] [2] [2] [2] [2] [2] [2] [2] [2] [2] [2	Dr. K. MDL, ANDZ/140; DADI4122.11	SULT 1( CJR3 C9LJ1 01-00 01-00 01-01 P101 P101	<pre>CC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; CC Brassicales; Brassicaceae; Arabidopsis. OX WCBL_TaxID=3702; RN [1] RP SEQUENCE FROM N.A. RP SEQUENCE FROM N.A. R2 STRAIN=COLOMBIA; RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.; R1 [2] R1 [2] R2 Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. R1 [2]</pre>	<pre>KC STRAIN=CULUMBLA; KC STRAIN=CULUMBLA; RA Nakamura Y :</pre>	DR PROSTER: PSOUDORS: MULARLEATE: UNANUMAL. DR ANART: SM00221; STYKC; 1. UNANUMAL. KW ATP-binding; Repeat; Transferase; WD repeat. SQ SEQUENCE 845 AA; 94353 MW; EBSAADEDFDI6F316 CRC64; Query Match 1.5%; Score 9; DB 10; Length 845; Best Local Similarity 100.0%; Pred. No. 3.3; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 523 SDDGTVKLW 531
<pre>FROM N.A. ESTIS; addit A., Lauber J., Mewes H.W., Gassen ad (JAN-2000) to the EMBL/GenBank/DDBJ ad 137748; CAB70903.1; ; IPR001609; ; IPR001609; 00400; WD40; 5. 02138; Beach; 2. PS50197; BEACH; 1. PS50197; BEACH; 1. ical protein. 524 AA; 58801 MW; F4A38C3EFE58D39</pre>	Query Match     Juength 5/4;       Best Local Similarity 100.08; Pred. No. 2.2;     District 100.08;       Matches     9; Conservative     0; Mismatches       Qy     357 VSGSRDATL 365     0; Mismatches     0; Indels     0; Gaps       Qy     357 VSGSRDATL 365       Db     318 VSGSRDATL 326       RESULT     8       Result     0       D0     09WW9       D0     09WW9	Q9WVM9; Q1-NOV-1999 (TEMBLrel. 12, Created) 01-NOV-1999 (TEMBLrel. 12, Last sequence 01-MAR-2001 (TEMBLrel. 16, Last annotatic LYSOSOMAL TRAFFICKING REGULATOR 2 (FRAGME LYST2. L		DR PROSTE: PS50197; BEACH; 1. DR SMART; SM00320; W40; 1. FT NOW_TER 1 1 1 SQ SEQUENCE 703 AA; 79349 WW; 5776B57B1D972127 CRC64; Query Match 1.5%; Score 9; DB 11; Length 703; Best Local Similarity 100.0%; Pred. No. 2.8; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 357 VSGSRDATL 365 11111111 Db 511 VSGSRDATL 519	RESULT 9 09H9K3 PRELIMINARY; PRT; 741 AA. TD 09H9K3 PRELIMINARY; PRT; 741 AA. AC 09H9K3; PRELIMINARY; PRT; 741 AA. DT 01HAR-2001 (TEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TEMBLrel. 16, Last annotation update) DT 01-MAR-2001 (TEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TEMBLREL 16, Last sequence 16, Last se

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RESULT 13 Q9EPM9	<pre>D 09EPM9 PRELIMINARY; PRT; 2931 AA. 09EPM9 PRELIMINARY; PRT; 2931 AA. DT 01-MAR-2001 (TrEWBLRE1 16, Created) DT 01-MAR-2001 (TrEWBLRE1. 16, Last sequence update) DT 01-MAR-2001 (TREWBLRE1. 16, Last sequence update) DE NEUROBEACHIN. NBEA. NBEA. OS Wus musculus (Mouse). NBEA. NAMMAIA; Eutheria; Condata; Craniata; Vertebrata; Euteleostomi; CC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; NBEA. NBEA</pre>	Query Match1.5%; Score 9; DB 11; Length 2931; Best Local Similarity 100.0%; Pred. No. 10; Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0; QY 357 VSGSRDATL 365 Db 2725 VSGSRDATL 2733No. 10; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 0; Mismatches 0; Indels 0; Gaps 0; Matches 0; Mismatches 0; Indels 0; Gaps 0;QY357 VSGSRDATL 365 IIIIII Db 2725 VSGSRDATL 2733RESULT 14	BEPNI BEPNI FEENIS FEENIS FEENIS FEENIS FEENIS BERNIS BERNIS BERNIS BERNIS FEENIS BERNIS BERNIS FEEN	9; Conservative 0; Mismatch SsRDATL 365 1111111 SSRDATL 2738
• bb 646 SDDGTVKLW 654	RESULT 11 09HCM8 PRELIMINARY; PRT; 1028 AA. 09HCM8 PRELIMINARY; PRT; 1028 AA. 00HCM8 PRELIMINARY; PRT; 1028 AA. 01HMR-2001 (TERBLrel. 16, Last sequence update) 01-MAR-2001 (TERBLrel. 16, Last annotation update) DT 01-MAR-2001 (TERBLrel. 16, Last annotation update) DT 01-MAR-2001 (TERBLREN]. EXAL1544 NIA1544 PROTEIN (FRAGMENT). DE KIAA1544 PROTEIN (FRAGMENT). C Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. C Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; C Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. C Mammalia: Eutheria; Primates; Catarrhini; Hominidae; Homo. RN [1] RP SEQUENCE FROM N.A. RN 1] RP SEQUENCE FROM N.A. RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NAG9Sef T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NA PAS T, RA NAG9SAF T, Kikuno R., Nakayama M., Hirosawa M., Ohara O.; RA NA RES 7:273-281(2000). RA NA RES 7:273-28	ate Mat	RESULT 12 09EPN0 ID Q9EPN0 DT 01-MAR-2001 (TrEMBLrel. 16, Created) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update) DT 01-MAR-2001 (TREMBLREL. DT 01-MAR-2001 (TREMBLREL. 16, Last annotation update) DT 01-MAR-2001 (TREMBLREL. 16, Last annotation update) DT 0100 (MULL 2000) DR 000 (MULL 2000) DR 00	Query Match1.5%; Score 9; DB 11; Length 2904;Best Local Similarity100.0%; Pred. No. 9.9;Matches9; Conservative0; Mismatches0;357 VSGSRDATL 3650p357 VSGSRDATL 3650p2698 VSGSRDATL 2706

066716 PRELIMINARY; PRT; 272 AA. 066716; 011-AUC-1998 (TEMBLRel. 07, Created) 01-AUC-1998 (TEMBLRel. 07, Last sequence update) 01-AUC-1998 (TEMBLRel. 13, Last annotation update) NUCHERTCAL 31.6 KDA PROTEIN. AUGIFS acollcus. Bacteria: Aquificales: Aquificaceae; Aquifex. NUCBL\_TaxID-63363; 11] SEQUENCE FROM N.A. SEQUENCE PROM N.A. SEQUENCE 272 AA; 31561 MW; 652D06C62E15D581 CRC64; CUENCE 272 AA; 31561 MW; 652D06C62E15D581 CRC64; SEQUENCE 272 AA; 31561 MW; 652D06C62E15D581 CRC64; SEQUENCE 272 AA; 31561 MW; 652D06C62E15D581 CRC64; ATTAND-TAXID NET NO.00, 0; Pred. NO. 13; Mature 38; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps

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copyright (c)	h, 25	5-09-328-877A-8 43 MSKPGKPTLNHGLVPVDLKS	M62 10.0 ,	é seds,	satisfying	00 1	um Match um Match ng first	eseq_0601 (1051/95996001) (1051/95996001) (1051/959960001) (1051/959960001) (1051/959960000000000000000000000000000000000	number an or eq Y analys	Length DB	00000000000000000000000000000000000000
Copy	protein searc September	US-09- 3143 1 MSKF	BLOSUM6 Gapop 1	41267	hits s		: Minimum Maximum Listing	Adema and a second seco	lo. is the reater th derived b	8 Query Match	100.0 100.0 99.99 92.0 92.0 92.0 92.0 92.0
	•	score: e:	table:	d:	number of	DB seq DB seq	Post-processing	 Φ	Pred. No. score grea and is den	Score	2890.5 2890.5 2890.5 2890.5 2890.5 2890.5 2890.5 2890.5
	OM protein Run on:	Title: Perfect Sequence	Scoring	Searched	Total nu	Minimum Maximum Doct.org	JJd-1SO4	Database	ar S S	Result No.	-100400F800

92.0 592 20 AAY22462 91.9 545 22 AAB59194 91.9 545 22 AAB59194 91.9 545 22 AAB59194 91.9 545 22 AAB59195 91.9 553 20 AAY22463 91.9 540 20 AAY22465 91.9 540 22 AAB59200 91.9 540 22 AAB59200 91.9 626 20 AAY22469 91.9 626 20 AAY22469 20.4 569 21 AAY83253 20.4 569 21 AAY83253 20.4 569 21 AAY83241 20.4 569 21 AAY83241 20.4 569 21 AAY83241 20.4 569 21 AAY83241	0.3 569 22 AAB48298 0.2 569 21 AAB12812 0.2 569 21 AAB12812 9.7 779 16 AAR85854 9.7 779 16 AAR85854 4.7 317 21 AAR85854 4.7 317 21 AAB63186 4.0 410 16 AAR70002 4.0 410 16 AAR70002 3.5 409 16 AAR70005 2.6 323 21 AAB63185	ALIGNMENTS andard; Protein; 589 AA. (first entry) ry sel-10 protein sequence. ap; presenilin; Alzheimer's diseas nd; therapy. ; 98WO-US268200. ; 98WO-US268200. ; 97US-0068239. ; 97US-0068239. Li J, Pauley AM; 58026/38. g9702. d human sel-10 polypeptides age 60-63; 91pp; English.
112 2890 114 2890 115 2899 116 2889 117 2889 2887 2889 2887 2887 223 2887 224 1238 641 641 640 640 640 640 640 640 640 640 640 640	5 4 4 4 6 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	LT 1 2466 stand AAY22466 stand AAY22466; Human mammry Sel-10; human; mammary gland; Homo sapiens. WO9932623-A1. 01-JUL-1999; 17-DEC-1998; 17-DEC-1997; (PHAA ) PHARMA Gurney ME, Li WPI; 1999-4580 N-PSDB; AAX997 New isolated h New isolated h

Human hippocampal Human bippocampal Human bippocampal Human bippocampal F-box protein Meta Amino acid sequenc F-box protein Neta Human beta-transdu Human beta-transdu Human beta-transdu Human beta-transdu Human beta-transdu Human cil sequenc F-box protein hBet Human cil signall Human secreted pro Human GTP-binding OPDE 45 kDa subuni OPDE 45 kDa subuni WD-40 domain-contg Gene 3 human secre

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<pre>XX FF 23-MAY-2000; 2000WO-USO9814. FF 09-JUN-1999; 99US-0328877. FAA ) PHARWACIA &amp; UPJOHN CO. XX Pauley AM, Gurney ME, Li J; Pauley AM, Gurney ME, Li J; Pauley AM, Gurney ME, Li J; WPI; 2001-102404/11. XX WPI; 2001-102404/11. XX WPI; 2001-102404/11. XX Vew human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide expression and as drug targets in the treatment of Alzheimer's disease restression and as drug targets in the treatment of Alzheimer's disease restression and as fung targets in the treatment of Alzheimer's disease restression and as fung targets in the treatment of Alzheimer's disease restression and as fung targets in the treatment of Alzheimer's disease restression antibody levels for detecting sel-10 polypeptide restression and useful for raising monoclonal or polyclonal restression and useful for detecting sel-10 polypeptides are useful for developting assays for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developting assays for identifying agents capable of with the biological pathways that lead to Alzheimer's disease. Sequence 589 AA; Sequence 589 AA;</pre>	Query MatchLocal Similarity100.0%;Score 3143;DB 22;Length 589;O;Matches 589;Conservative0;Mismatches0;Tadeis0;Gaps0;Matches 589;Conservative0;Mismatches0;Tadeis0;Gaps0;Matches 589;Conservative0;Mismatches0;Tadeis0;Gaps0;D1Miskegkpthingiuputputtersinteunocuperstrankindhese0;Estsigkpckvseytsttgiupediatentifsisiliagilf(111111111111111111111111111111111111
CC This sequence represents a human sel-10 protein of the invention. This ecc sequence is specifically a human mammary sel-10 protein. The polypetides cc the expression or the activity of the human sel-10 proteptides may cc the expression or the activity of the human sel-10 polypetides cc therefore may be useful for the presentin-1 (PS-1) or PS-2, and dc therefore may be useful for the prevention or treatment of Alzheimer's disease	<pre>Qy 211 HRIDTWWRRGELKSFYVLKGHDDHVITCLQFCGNRIY9SGSDNTLKYWSAVTGKCLFTLV 300 Db 241 httdrwrrgelkspkvlkyddnvltc.lqfcgnriy9gddntlkywwsryckClrtlv 300 dy 301 GrTGCWMSSQMRDNIIISGSTDFTLKYWNAFGGCTHFLYGHTSYVRCMHLMEKRVYSGS 360 d) 301 ghtggrwssqmrdnii1gssrdnrikywnafggcclhhlyghtetvrramhhkrivvggs 360 301 ghtggrwssqmrdnii1gssrdnrikywnaergeelhhlyghtetvramhhkrivvggs 360 301 ghtggrwssqmrdnii1gssrdnrikywnaergeelhhlyghtetvramhhkrivvggs 360 302 fbrfGVWSSQMRDNIIISGSTDFTLKWNNAEFGGCTHFLYGHTSYVSCNHLMEKRVYSGS 360 303 ghtggrwssqmrdnii1gssrdnrikywnaergeelhhlyghtetvramhhkrivvggs 360 303 ghtggrwssqmrdnii1gssrdnrikywnaergeelhhlyghtetvramhhkrivvggs 360 304 21 ghtlivvdletggclhvinghwaavrevgydgrrvysgaydfmvkwdpetetclhtig 420 305 fadatlrvwdletggclhvinghwaavrevgydgrrvysgaydfmvkwdpetetclhtig 420 304 21 ghtlivvdletggclhvinghwaavrevgydgrrvysgaydfmvkwdpetetclhtig 420 305 fadatlrvwdletggclhvinghwaavrevgydgrrvysgaydfmvkwdpetetclhtig 420 307 421 GHTNNYSLDCDCHNCOCPURCNENTERSENSCHELKDNII/11111111111111111111111111111111111</pre>

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121 121 181 181 241 241	<pre>0y 301 GHTGGWSSQMRDNIIISGSTDFTLKWNAETGECIHTLYCHTSTVRCMHLHEKRVYSGS 360 111111111111111111111111111111111111</pre>	Qy541 NLVTLESGGGGVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDWK 58911111111111111111111111111111111111	<pre>Sel-10; human; presenilin; Al mammary gland; therapy. Homo sapiens. W09932623-Al. 01-JUL-1999, 98WO-US26820. 17-DEC-1998; 97US-0068243. 19-DEC-1997; 97US-0068243. (PHAA ) PHARMACIA &amp; UPJOHN CO Gurnev ME. Li J., Paulev AM:</pre>	WPI: 1999-458026/38. W-PSDB; AAX99702. New isolated human sel-10 Claim 24; Page 63-66; 91pr This sequence represents a sequence is specifically a can be used to alter prese the expression or the activity the expression or the activity of mut
<pre>Db 541 nlvtlesggsggvvwrirasntklvcavgsrngteetkllvldfdvdmk 589 RESULT 3 AAB01204 ID AAB01204 standard; Protein; 589 AA. XX AAB01204; XX 03-NOV-2000 (first entry) DT 03-NOV-2000 (first entry) DT 03-NOV-2000 (first entry) DT 03-NOV-2000 (first entry) DT 03-NOV-2000 (first entry)</pre>	<pre>Guanine nucleotide binding protein; GTP-binding protein; G-protein; GTPase: GTPase associated protein; GTPAP; cell proliferation; autoimmune; inflammatory; immune system disorder; cancer; AIDS; acquired immune deficiency syndrome; asthma; atherosclerosis; arthritis; systemic lupus erythematosus; psoriasis; human. Homo sapiens. W0200031263-A2. 02-JUN-2000. 23-NOV-1999; 99W0-US28013.</pre>	<pre>Journary 2005.0118610. 04-FEB-1999; 99US-0118610. 06-APR-1999; 99US-0127990. (INCY-) INCYTE PHARM INC. Hillman JL, Tang YT, Bandman O, Lal P, Yue H, Lu DAM, Baughn MR; Yang J, Azimzai Y; WPI; 2000-400073/34. WPI; 2000-400073/34. N-PSDB; AAA49199. Human GTPase associated proteins, polynucleotides, and antibodies, useful for diagnosing, preventing and treating various diseases such as atheroscierosis, cancer, acquired imune deficiency svndrome (AIDS).</pre>		Similan B; Cou PGKPTLI PGKPTLI PGKPTLI PGKPTLI SLGKKPC SLGKKPC

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<pre>XX Pauley AM, Gurney ME, Li J; XX WFI; 2001-102404/11. XX WFI; 2001-102404/11. FT Wew human sel-10 polypeptides and their encoding polynucleotides, PT Useful for raising antibodies for detecting sel-10 polypeptide PT USEFUL for raising antibodies for detecting sel-10 polypeptide PT USEFUL I; Page 83-86; 116pp; English. XX The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of the thological pathways that lead to Alzheimer's disease. XX Sequence 559 AA;</pre>	Query Match94.9Best Local Slmilarity100.Matches559; Conservative31 MKIFSISIIA0GLPFCRRMM11111111111111111111111111111111111	QY571 RNGTEETKLLVLFDVDMK 589D11111111111111111D541 rngteetkilvldfdvdmk 559RESULT6AAY22461tandard; Protein; 627 AA.
<pre>CC disease. XX Sequence 559 AA; Ouery Match 94.9%; Score 2983; DB 20; Length 559; Best Local Similarity 100.0%; Pred. No. 4.6e-283; Matches 559; Conservative 0; Mismatches 0; Indels 0; Gaps 0; 0y 31 MKIFSISIIAQGLFFCRRMKRLDHGSEVRSFSLGKKPCKVSEYTSFTGLVPCSATFT 90 [111111111111111111111111111111111111</pre>	0y271FCGNRIYGSGSDWTLKVWGAVTGKCLRFLVCHTGGVWSSOMRDNIIISGSTDRFLKVWNA300100241EGGITLYGSGSDWTLKVWGAVTGKCLRFLVGH111111111111111111111111111111111111	XX PD 14-DEC-2000. XX PF 23-MAY-2000; 2000WO-US09814. XX XX PA (РНАА ) РНАЕМАСІА & UPJOHN CO.

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C AAY22461;	QY 397 VSGAYDPMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCI 456
7 29-SEP-1999 (first entry)	Db 435 vsgaydfmvkvwdpetetclhtlqghtnrvyslqfdg1hvvsgsldtsirvwdvetgnci 494
B. Human hippocampal sel-10 protein seguence.	QY 457 HTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNK 516
A Sel-10; human; presenilin; Alzheimer's disease; PS-1; PS-2; hippocampus; W therapy	Db 495 htltghqsltsgmelkdnilvsgnadstvkiwdiktggclqtlqgpnkhqsavtclqfnk 554
	QY 517 NFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGCVVWRIRASWTKLVCAVGSRNGTEE 576
6 D D C M	Db 555 nfvitssddgtvklwdlktgefirnlvtlesggsgggyvwrirasntklvcavgsrngtee 614
	QY 577 TKLLVLDFDVDMK 589
tx эғ 17-DEC-1998; 98WO-US26820.	Db 615 tklivldfdvdmk 627
XX PR 19-DEC-1997; 97US-0068243.	RESULT 7
KX PA (PHAA ) PHARMACIA & UPJOHN CO.	93 AB5
XX PI Gurney ME, Li J, Pauley Ам;	AAB59193;
XX WPI; 1999-458026/38. Dr scret arvoo701/	XX DT 23-MAR-2001 (first entry)
	DE Human hippocampal sel-10-1 protein.
-	XW Sel-10; human; Alzheimer's disease; Abeta.
	XX OS Homo sapiens.
CC This sequence represents a human sel-10 protein of the invention. This sequence is specifically a human hippocampal sel-10 protein. The	W0200
polypeptides can be used to alter presentin function. Compounds inhibit either the expression or the activity of the human sel-10	XX PD 14-DEC-2000.
	XX PF 23-MAY-2000; 2000WO-US09814.
-	XX PR 09-JUN-1999; 99US-0328877.
sequence b2/ AA;	XX PA (PHAR ) PHARMACIA & UPJOHN CO.
0%; Score 2890.5; DB 20; Length 627; 9%; Pred. No. 6.3e-274;	Paule
L SUISELVALIVE	DR WPI; 2001-102404/11. xx
<pre>Qy 13 LVPVDLKSAKEPLPHQTVMKIFSISIIAOGLPFCRR</pre>	PT New human sel-10 polypeptides and their encoding polynucleotides, PT useful for raising antibodies for detecting sel-10 polypeptide PT expression and as drug targets in the treatment of Alzheimer's disease
Qy         49        RWKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRA         96           :111111111111111111111111111111111111	PT - XX PS Claim 1; Page 60-64; ll6pp; English. XX
ANGGOORREITSVOPPTGLOGWLKNEOSWSCPEKLLALDELEDSGEPFOURGEWANDVER ANGGOORREITSVOPPTGLOGWLKNEOSWSCPEKLLALDELEDSGEPFOURGEWANDVER 111111111111111111111111111111111111	CC The present invention relates to human sel-10. The sel-10 proteins of CC the invention are useful for raising monoclonal or polycional CC antibodies useful in diagnostic assays for detecting sel-10 CC polycoptide expression. The sel-10 polycoptides are also useful as drug
Oy         157         OFQRDFISLLPKELALYVLSFLEPKDLLQAAOTCRYWRILAEDNLLWREKCKEEGIDEPL         216         111111111111111111111111111111111111	CC targets for decreasing antibody levels in the treatment of Alzheimer's CC disease. It is also useful for identifying agents capable of CC altering the production level of Abeta. The polynucleotides are useful CC for developing assays for identifying agents capable of interfering
<pre>Qy 217 HIKRRKVIKPGFIHSPKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRI 276 1                                    </pre>	
Qy         277         VSGSDDNTLkVWSAVTGKCLRTLVGHTGGWSSOMRDNIIISGSTDRTLKVWNAETGECI         336         111111111111111111111111111111111111	Query Match 92.0%; Score 2890.5; DB 22; Length 627; Best Local Similarity 89.9%; Pred. No. 6.3e-274; Matches 551; Conservative 11; Mismatches 10; Indels 41; Gaps
Qy         337         HTLYGHTSTVRCMHLHEKRVVSGSRDATLRVMDIETGQCLHVLMGHVAAVRCVQYDGRRV         396         111111111111111111111111111111111111	Qy       13       LVPVDLKSAKEPLPHQTVMKIFSISIIAOGLPFCRR

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<pre>49PNKFKLOHGSEVBEFSELKKFCVVSEYTSTTGLVCGATPTTFFOLLAG 75 mgfygtLkmifymkrkidhgsevrsfiljiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii</pre>
49           135           137           147  <

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human	
isolated	5)35200
New	;

- Page 85-88; 91pp; English Example 3;
- This sequence is an epitope-tagged version of a human sel-10 protein of the invention. The human sel-10 proteins of the invention are isolated from hippocampus and mammary gland. The polypeptides can be used to alter presentlin function. Compounds which inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presentlin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of Alzheimer's disease.
- 666 AA; Sequence

	ba	48	74	96	134
	Ga	1	en	RA	ra -
666;	41;		kgknt	TFGDL	tfgdl
92.0%; Score 2890.5; DB 20; Length 666; 89.9%; Pred. No. 7e-274;	Matches 551, Conservative 11; Mismatches 10; Indels 41; Gaps	13 LVPVDLKSAKEPLPHQTVMKIFSISIIAQCLPFCRR	20 llpvllpnlpfltclsmstlesvtylpekgl-ycgrlpssrthggteslkgknten 74	RMKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRA 96	75 mgfygtlkmifykmkrkldhgsevrsfslgkkpckvseytsttglvpcsatpttfgdlra 134
DB 20; 274:	10;	CRR	I:I cqrlpssr	EYTSTTGL	eytstgl
92.0%; Score 2890.5; DB 89.9%; Pred. No. 7e-274;	smatches		: 11 : Lpekgl-y(	SKKPCKVS	Jkkpckvs
Score Pred.	11; Mis	SISIIA-	tlesvtyl	EVRSFSLO	evrsfslg
	ative	HQTVMKIF	fltclsms	KRKLDHGS	krkldhgs
Query Match Best Local Similarity	Conserv	KSAKEPLP	lipvlipnlpfitclsmstlesvtylpekgl-ycgri	RM	lkmifykm
atch cal Sim	551;	LVPVDL	llpvll	49 49	mgfygt
Query Match Best Local S	atches	13	20	49	75
ŌĂ	Ÿ	Qγ	Db	οy	qq

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- 156 216 194 **QFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPL** 97 135 157 qq Qγ Qγ
  - 254 195
- 276 HIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRI 217 оу ОУ
  - 314 255
  - Db QY
- 336 VSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECI 277
  - 374 315 đ
- 396 337 QУ
  - 434 375 q
- 456 VSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCI 397

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HTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNK

TKLLVLDFDVDMK 589

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C-terminal mychis tagged sel-10 protein.

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RESULT AAB59203 ID AAB5 XX AC AAB5 XAC AAB5 XX DT 23-M XX DT 23-M DE C-te

NFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEE

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XX		Db 435 vsgaydfmvkvwdpetetclhtlgghtnrvyslqfdgihvvsgsldtsirvwdvetgnci 494
XX	Set-IU; Numan; Alzneimer's disease; Abeta.	
SO XX	Homo sapiens.	
Nd	W0200075328-A1.	C
D d	14 - DEC - 2000.	ŝ
AX PF	23-MAY-2000; 2000WO-US09814.	
XX R H	09-JUN-1999; 99US-0328877.	577
XX PA	(PHAA ) PHARMACIA & UPJOHN CO.	Db 615 tklividfavamk 627
AX FI	Pauley AM, Gurney ME, Li J;	RESULT 10
	WPI; 2001-102404/11.	AAY22470 ED AAY22470 standard; Protein; 669 AA.
A T T	New human sel-10 polypeptides and their encoding polynucleotides, useful for raising antibodies for detecting sel-10 polypeptide	XX AC AAY22470; XX
	in	27 29-SEP-1999 (first entry) XX
	Example 3; Page 108-112; 116pp; English.	
	The present invention relates to human sel-10. The sel-10 proteins of	KW Sel-10; human; presentlin; Alzheimer's disease; PS-1; PS-2; hippocampus; KW therapy; mammary gland.
	antibodies useful in diagnostic assays monocional or polycional polypeptide expression. The sel-10 polypeptides are also useful as drug	xx DS Homo sapiens. DS Synthetic.
	targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of	
	altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering	
	with the blological pathways that lead to Alzheimer's disease.	XX PF 17-DEC-1998; 98WO-US26820.
		XX PR 19-DEC-1997; 97US-0068243.
Que	Query Match 92.0%; Score 2890.5; DB 22; Length 666; Bact Loral similarity 20.0%, Bood Wo 72-274	(PHAA ) PHARMACIA & UPJOHN CO.
Mat	vative ]	AX PI Gurney ME, Li J, Pauley AM;
Qγ	13 LVPVDLKSAKEPLPHOTVMKIFSISIIAQGLPFCRR48  :    :     : :::: : : : :     :	XX DR WPI; 1999-458026/38. DA - Decre: aavoo715
qq	20 lipvilpnlpfitcismstiesvtylpekgi-ycqripssrthggtesikgknten 74	
vo 40	49RMKRKLDHGSEVBSFSLGKKPCKVSEYTSTTGLVPCSATPTTGDLRA 96 75 mcfurt1bm16.ubbr/1340000006134111111111111111111111111111	PT New isolated numan sel-10 polypeptides PS Example 3; Page 79-83; 91pp; English.
2 2	wyryscramatywwrthunysevisisigkkpcKvseycsCigivpcsacpCLfgdlfa амслоловрттеуллрингтуры умолоногтырттататал	This sequence is an epitope-tagged
6 q	11111111111111111111111111111111111111	
QY		3.C or the activity of the human sel-10 polypeptides may reverse the effects 2.C of mutations to presentilin-1 (PS-1) or PS-2, and therefore may be useful 2.C for the prevention or treatment of Alzheimer's disease.
qq	195 qfqrdfisllpkelalyvlsflepkdilgaaqtcrywrilaednliwrekckeegidepl 254	
vo bb	217 HIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPRVLKGHDHVITCLQFCGNRI 276 	Dierv Match 92 0%:
QY	VSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECI	Similarity 89.9%, Pred. No. 7574; Conservative 11; Mismatches 10; Indels
qq		LVPVDLKSAKEPLPHQTVMKIFSISIIAQGLPFCRR48
QY		1:11     1:1     1:1:1       Db     20     11pvllpnlpfltclsmstlesvtylpekgl-ycgrlpssrthggteslkgknten
qa	375 htlyghtstvrcmhlhekrvvsgsrdatlrvwdietggclhvlmghvaavrcvqydgrrv 434	Qy 49RMKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRA 96 :
oy .	397 VSGAYDFWVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSTRVWDVETGNCI 456	Db 75 mgfygtlkmifykmkrkldhgsevrsfslgkkpckvseytsttglvpcsatpttfgdlra 134

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SVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEP 156 	21 25 25	HIKKKVIKPGFIKSPWKSATIROHRIDTMMRRGELKSPKVLKGHDHVITCLQFCGNRI 276 	VSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECI 336 	HTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRV 396 	DFWVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCI 456 	TSGMELKDNILVSGNADSTVKIMDIKTGOCLQTLQGPNKHQSAVTCLQFNK 516 	SSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEE 576 	589 627	<pre>ird; protein; 669 AA. ilrst entry) ils tagged sel-10 protein. Alzheimer's disease; Abeta. alzheimer's disease; Abeta. 00WO-US09814. 99US-0328877. ifA &amp; UPJOHN CO. iTA &amp; UPJOHN CO. iTA &amp; UPJOHN CO. iTA &amp; UPJOHN CO. iTA &amp; UPJOHN CO. iney ME, Li J; M/11. 0 polypeptides and their encoding polynucleotides, ing antibodies for detecting sel-10 polypeptide as drug targets in the treatment of Alzheimer's disease as drug targets in the treatment of Alzheimer's disease inflon relates to human sel-10 the sel-10 proteins of fortion relates to human sel-10 the sel-10 proteins of</pre>
ANGQGQQRRRIT            angqgqqrrrit	r 5 r	~ 5			VSGAY       vsgay	HTLTGHOSL           htltghgsl	NFVIT       nfvit	TKLLV       tkllv	<pre>11 59202 standard; 59202; MAR-2001 (first erminal v5 His t erminal v5 His t erminal v5 His t erminal v5 His t onoo75328-A1. 00075328-A1. 00075328-A1. 00075328-A1. 00075328-A1. 00075328-A1. 00075328-A1. 000715328-A1. 000715328 000715328-A1. 000715328 000715328 000715328-A1. 000715328 000715328-A1. 000715328-A1. 000715328-A1. 000715328 000715328-A1. 000715328 000715328-A1. 000715328 000715328-A1. 000715328 000715328-A1. 000715328 000715328 000715328 00071532 00071532 00071532 00071532 00071532 0001102404 00 0007153 0001 0018 000 001315 000 001 001 001 001 001 001 001 001 0</pre>

the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as drug targets for decreasing antibody levels in the treatment of Alzheimer's disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful for developing assays for identifying agents capable of interfering with the biological pathways that lead to Alzheimer's disease.	Query Match 92.0%; Score 2890.5; DB 22; Length 669; Best Local Similarity 89.9%; Pred. No. 7e-274; Matches 551; Conservative 11; Mismatches 10; Indels 41; Gaps	<pre>13 LVPVDLKSAKEPLPHQTVMKIFSISIIAQGLPFCRR</pre>	49RKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRA 96 :	97 ANGGGGORRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTOVKHMMOVIEP 156 	157 QFORDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPL 216 	217 HIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRI 276 	277 VSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECI 336 	337 HTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRV 396 	397 VSGAYDFMVKVWDFETETCLHTLQGHTNRVYSLQFDGTHVVSGSLDTSIRVWDVETGNCI 456 	457 HTLTGHQSLTSCMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNK 516 	VTLESGGSGGV             Vtlesggsggv	77 TKLLVLDFDVDMK 589               15 tkllvldfdvdmk 627	JLT 12 22462 AAY22462	29-SEP-	Human hippocampal sel-10 protein sequence.	<pre>Sel-10; human; presention; Alzheimer's disease; PS-1; PS-2; hippocampus; therapy.</pre>
8555555555588	Omz	b Q	чо Бр	QY Db	оу вр	ч р о	ъ д	δ d	оy Db	D D D	оу Db	QY Db	RESI AAY: XX	XE	XBX	KW

<pre>Qy 542 LVTLESGCSGCVVWRIRASWIKLVCAVCSRNGTEETKLLVLDFDVDWK 589 111111111111111111111111111111111111</pre>	RESULT 13	AAB59194 ID AAB59194 standard; protein; 592 AA.	XX AC AAB59194;	XX DT 23-MAR-2001 (first entry)	XX DE Human hippocampal sel-10-2 protein.	XX KW Sel-10; human; Alzheimer's disease; Abeta. XX	OS Homo sapiens. XX		PD 14-DEC-2000. XX PF 23-MAY-2000; 2000WO-US09814. XX	PR 09-JUN-1999; 99US-0328877. XX PA (PHAA ) PHARMACIA & UPJOHN CO.	AX PI Pauley AM, Gurney ME, Li J; XX DR WPI: 2001-102404/11.	New h usefu expre	- Claim 1; Page 64-68; ll6pp; English.	The present invention relates to human sel-10. The sel-10 proteins the invention are useful for raising monoclonal or polyclonal antibodies useful in diagnostic assays for detecting sel-10 polypeptide expression. The sel-10 polypeptides are also useful as	CC targets for decreasing antibody levels in the treatment of Alzheimer's CC disease. It is also useful for identifying agents capable of CC altering the production level of Abeta. The polynucleotides are useful CC for developing assays for identifying agents capable of interfering		Query Match 92.0%; Score 2890; DB 22; Length 592; Best Local Similarity 93.4%; Pred. No. 6.5e-274; Matches 549; Conservative 3; Mismatches 10; Indels 26; Gaps	Qy       2       SKPGKPTLNHGLVPVDLKSAKEPLPHQTVMKIFSISIIAQGLPFCRRMKRKLDHGSEVR 61         Qy       2       SKPGKPTLNHGLVPVDLKSAKEPLPHQTVMKIFSISIIAQGLPFCRRMKRKLDHGSEVR 61         D       1       1       1         Db       31       slkgkntenmgfygtlkmifygtlkmifygtlkmifygknkrkldhgsevr 64	RAANGQGQQRRR              raangqgqqrrr	Qy         122         MFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKELALVVLSFLEPK         181         111111111111111111111111111111111111	
		98WO-US26820.	97US-0068243.	& UPJOHN CO.	Pauley AM;		sel-10 polypeptides	91pp; English.	ts a human sel-10 protein of the invention. This 17 a human hippocampal sel-10 protein. The ed to alter presentin function. Compounds which	inhibit either the expression or the activity of the human sel-10 polypeptides may reverse the effects of mutations to presenilin-1 (PS-1) or PS-2, and therefore may be useful for the prevention or treatment of		92.0%; Score 2890; DB 20; Length 592; Larity 93.4%; Pred. No. 6.5e-274; Conservative 3; Mismatches 10; Indels 26; Gaps 2;	<pre>SKPGKPTLNHGLVPVDLKSAKEPLPHQTVMKIFSISIIAQGLPFCRRRMKRKLDHGSEVR 61                                      </pre>	RAANGGGQQRRRITSVQPPTGLQEWLK                                *aangggggrrfitstgppfglgewlk	MFQSWSGFEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLEPK 181 	DLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGFIHSPWKSAYIRQH 241 	RIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVG 301 	HTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSR 361 	DATLRVWDIETGOCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTLQG 421 	HTNRVYSLQFDGIHVVSGSLDTSIRVMDVETGNCIHTLTGHQSLTSGMELKDNILVSGNA 481 	DSTVKIMDIKTGOCLOTLOGPNKHOSAVTCLOFNKNFVITSSDDGTVKLMDLKTGFFIRN 541

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QY	49	RMKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGGGQQRRRIT 108
qq	ۍ ۱	
οy	109	SVOPPTGLOEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPK 168
qq	65	vqpptglqewlkmfqswsgpekllaldelidsceptqvkhmmqviepqfgrdflsllp
QY -	169	2 3
q	125	elalyvistlepkdilgaaqtcrywrilaednilwrekckeegidepinikrrkvikpgr 184
σy	229	IHSPMKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVW 288
qq	185	inspwksayirghridtnwrrgelkspkvlkghödhvitcigfcgnrivsgsddntlkvw 244
οy	289	SAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRC 348
qq	245	savtgkclrtlvghtggvwssqmrdniiiisgstdrtlkvwnaetgecihtlyghtstvrc 304
οy	349	MHLHEKRVVSGSRDATLRVMDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVW 408
qa	305	millillillillillillillillillillillillill
QY	409	DPETETCLHTLQGHTNRVYSLQFDGTHVVSGSLDTSIRVMDVETGNCIHTLTGHQSLTSG 468
qq	365	detetclhtlightnrvyslgfdgihvvsgsldtsirvwdvetgncihtltghgsltsg 424
QY	469	MELKDNILVSGNADSTVKIMDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTV 528
qQ	425	melkdnilvsgnadstvkiwdiktggclqtlggpnkhgsavtclqfnknfvitssddgtv 484
QY	529	KLMDLKTGEFIRNLVTLESGGSGGVVMRLRASNTKLVCAVGSRNGTEETKLLVLDFDVDM 588
dq	485	treater and the second s
QY	589	K 589
qq	545	k 545
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X	ש ר	110 Stallagter, protectil, J40 AM.
XX		
T X X	23-MAI	.R-2001 (first entry)
303	Human hi	hippocampal sel-10-4 protein.
KW X	Sel-1	.0; human; Alzheimer's disease; Abeta.
v s	Ното	sapiens.
NA	WO200	00075328-Al.
XX Dd	14-DEC	sc - 2000 .
PF	23-MA	XY-2000; 2000WO-US09B14.
XX PR	זנ-60	JUN-1999; 99US-0328877.
XX PA	( РНАА	V ) PHARMACIA & UPJOHN CO.
¥I3	Paule	ey AM, Gurney ME, Li J;
<b>3</b> 23	(IAW	2001-102404/11.
54 LA	New hui useful expres:	human sel-10 polypeptides and their encoding polynucleotides, ul for raising antibodies for detecting sel-10 polypeptide ession and as drug targets in the treatment of Alzheimer's disease

PT -XX Claim 1; Page 72-75; 116pp; English. XX The present invention relates to human sel-10. The sel-10 proteins of CC The present invention relates to human sel-10. The sel-10 proteins of the invention are useful for raising monoclonal or polyclonal CC antibodies useful in diagnostic assays for detecting sel-10 CC antibodies useful in diagnostic assays for detecting sel-10 CC disease. It is also useful for identifying agents capable of altering the production level of Abeta. The polynucleotides are useful vith the biological pathways that lead to Alzheimer's disease. XX Sequence 545 AA;

ö IHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTLKVW 288 49 RMKRKLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRIT 108 109 SVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPK 168 228 244 SAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRC 348 304 408 364 468 424 MELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTV 528 484 588 544 Gaps 64 485 klwdlktgefirnlvtlesggsggvvwrirasntklvcavgsrngteetkllvldfdvdm ELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGF MHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVW DPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSG 365 dpetetclhtlgghtnrvyslqfdgihvvsgsldtsirvwdvetgncihtltghqsltsg KLWDLKTGEF IRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFDVDM ; 0 Length 545; Indels 91.9%; Score 2889; DB 22; 99.8%; Pred. No. 7.1e-274; cive 1; Mismatches 0; Query Match 91.9 Best Local Similarity 99.8 Matches 540; Conservative 589 K 589 k 545 125 65 169 229 289 245 305 425 529 545 349 409 469 q g g ą q qq δ qq δ g à 5 δ δ δ 2 δ qq δ g

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28       272.5       8.7       340       1       US-08-190-802A-42       Sequence 42, Appl         29       269.5       8.6       325       1       US-07-626-589-2       Sequence 2, Appl         30       269.5       8.6       325       1       US-08-190-802A-57       Sequence 57, Appl         31       269.5       8.6       325       1       US-08-190-802A-57       Sequence 57, Appl         31       269.5       8.6       325       1       US-08-123-44A-1       Sequence 1, Appl         32       269.5       8.6       325       1       US-08-326-410-2       Sequence 2, Appl         33       269.5       8.6       325       1       US-08-421-2       Sequence 2, Appl         34       269.5       8.6       325       1       US-08-421-2       Sequence 2, Appl         34       265       8.6       325       1       US-09-465-421-2       Sequence 2, Appl         35       265       8.4       31       05-08-465-410-2       Sequence 2, Appl         35       265       8.4       31       05-09-65-400-1       Sequence 2, Appl         36       265       8.4       32       105-09-665-600-1       Sequence 2, App	256         B.1         2627         2         US-08-751-189-3         Sequence 3,           256         B.1         2627         2         US-09-060-836-3         Sequence 3,           256         B.1         2627         2         US-09-184-445-3         Sequence 3,           253         B.0         340         1         US-08-190-802A-40         Sequence 40,           250         B.0         340         1         US-08-190-802A-40         Sequence 40,	246.5         7.8         317         1         US-08-190-802A-27         Sequence           246.5         7.8         317         1         US-08-190-802A-41         Sequence           246.5         7.8         317         1         US-08-190-802A-41         Sequence           246.5         7.8         317         1         US-08-190-802A-41         Sequence	ALIGNMENTS		plication US 17153 WATION:	APPLICANT: Greenwald, Iva APPLICANT: Hubbard, E. Jane TITLE OF INVENTON: SEL-10 AND USES THEREOF NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSEE: COOPER & DUNHAM LLP STREET: 1185 Avenue of the Americas CITY: New York	STATE: New York COUNTRY: U.S.A. ZIP: 10036 CONDTER READABLE FORM:	MEDIUM TIFE: FIOPPY DISK ; COMPUTER: IBM PC compatible ; ODPDATING SVETEM PC compatible	CURRENT AFPLICATION DATA: US Version #1.30 CURRENT APPLICATION DATA:	FILING DATE: US/U8/899,5/8 FILING DATE: 24-JUL-1997 CLASSIFICATION: 435 ATPORNEY/AGENT INPORMATION:	REGISTRATION NUMBER: 28,678	<pre>preference/Docket number: 0575/53200/JFW/AKC preferencertion information:</pre>	; TELEPHONE: (212) 278-0400 ; TELEFAX: (212) 278-0525	; INFORMATION FOR SEQ ID NO: 2: ; SEQUENCE CHARACTERISTICS:	; LENGTH: 587 amino acids ; TYPE: amino acid	TOPOLOG MOLECULE		Query Match 39.4%; Score 1238; DB 3; Length 587;	les 262; Conservative 85	55 DHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRANGGGQQRRRITSV 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1 1:1	15	QY 111 QPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKEL 170
GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. OM protein - protein search, using sw model Run on: September 25, 2001, 14:39:00 ; Search time 13.65 Seconds (without alignments) 888.477 Million cell updates/sec	score: e:	Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Searched: 107330 secs 20500316 rocidinos	mber of hits satisfying chosen	Minimum DB seq length: 0 Maximum DB seq length: 200000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	<pre>Database : Issued_Patents_AA:*     1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*     2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*     3: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*     5: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*     6: /cgn2_6/ptodata/2/iaa/bacKfiles1.pep:*</pre>	Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	8 SUMMARIES	Result Query . No. Score Match Length DB ID Description	1238 39.4 587 3 US-08-899-578-2 Sequen 671 21.3 209 3 US-08-899-578-6 Sequen 623 19.8 517 1 US-08-190-802A-30 Sequen	618.5 19.7 779 1 US-08-190-802A-32 • Sequence 32 439 14.0 409 2 US-08-283-917-3 Sequence 3,	439 14.0 409 2 US-08-961-716-3 Sequence 3, 439 14.0 410 2 US-08-283-917-9 Sequence 9,	439 14.0 410 2 US-08-961-716-9 Sequence 9, 424.5 13.5 409 1 US-08-190-802A-51 Sequence 51,	410 13.0 212 3 US-08-899-578-7 Sequence 7, 376.5 12.0 422 1 US-08-190-802A-52 Sequence 52,	<b>364.5 11.6 514 1 US-08-190-802A-66 Sequence 66</b> <b>332 10.6 704 1 US-08-188-582-5 Sequence 5</b> ,	332 10.6 704 1 US-08-646-715-5 Sequence 326 10.4 704 1 US-08-190-802A-62 Sequence	326 10.4 704 2 US-08-308-818-3 Sequence 3, 319.5 10.2 713 1 US-08-190-802A-63 Sequence 63	JL.5 10.1 704 1 US-00-189-582-18 Sequence 317.5 10.1 704 1 US-00-646-715-18 Sequence 311.5 9.9 375 4 US-00-664-713-1 Sequence	306 9.7 798 1 US-08-190-802A-64 Sequence 64 306 9.7 798 1 US-08-190-802A-64 Sequence 64	9.7 798 2 US-08-308-818-2 Sequence 2, 9.2 318 1 US-08-190-802A-33 Sequence 33 9.1 016 1 US-08-100-002A-33 Sequence 33	280.5 8.9 340 1 US-08-190-902A-31 Sequence 280.5 8.9 340 1 US-08-190-802A-38 Sequence	2/0 8.8 340 4 US-09-180-783-2 Sequence 2,

a o	//VENLIANEADEADAAAFIRLUGESUMINIKULKAIIEFHEURUFISCEFVEL 131 171 ALYVLSFLEPRDLLQAAOTCRYWRIIAEDNLLWREKCKEE210	us-08-899-578-6
ov b 1	: :        :    : ::::  : : :    GMKILHNLTGYDLLKVAQVSKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAI GIDEPLHIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVL	Query Match 21.3%; Score 6 Best Local Similarity 52.2%; Pred. N Matches 145; Conservative 24; Mism
qq	:       :       :       :       :     : :   : :   : :   :	QY 260 GHDDHVITCLQFCGNRIVSGSDDNTLKVWSA
γο 4	KGHDDHVITCLOFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSOMRDNII :       : : : : : : : : : : : : : : : :	1
a Vo	232 KGHEUHYTTCMQIHUDVLVIGSUDNTLKYWCIDKGEVMTILVGHTGGVWTSQLSQLSQCGRYI 311 317 ISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCL 376	QY 3.18 SGSTDRFLKWMARTGECLHTLVGHTSTVK 1
qq	:       :   :  :   :  :          : :: :	QY 378 VLMGHVAAVRCVQYDGRRVVSGAYDFMVKVW
оy	377 HVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVMDPETETCLHTLQGHTNRVYSLQFDGIH- 435	Db 91GHHAAVRCVQFDGTTVVSGGYDFTVKIW
a d	ATLHGHHAAVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLFGHNNRVYSLLFESERS	436 VVSGSLDTSIRVWDVETGNCIHT
D D	436 -VVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIMDIK 491 1	Db 137 VCSGSLDTSIRVWDGHTSL7 QY 496 LQTLQGPNKHQSAVTCLQ-FNKNFVITSSDC
yo d	492         TGQCLQTLQGPNKHQSAVTCLQ-FNKNEVITSSDDGTVKLMDLKTGEFIRNLVTLESGGS         550           1 </td <td>Db 180GHRSAITSLQWFGRNMVATSSDC</td>	Db 180GHRSAITSLQWFGRNMVATSSDC
δ i	GCVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFD 585    :  : :::                :::	RESULT 3 US-08-190-802A-30 ; Sequence 30, Application US/08190802A
3	000 DATA DOCUMENTATION AND A DOCUMENTATION DOCUMENTO DOCUMENTATION DOCUMENT	FALGUL NO. 3319003 GENERAL INFORMATION: APPLITCANT: MOCHUV-ROSEN, Daria
RESU US-0 : Se	RESULT 2 US-098-99-578-6 : Sequence 6, Application US/08895578	APPLICANT: Ron, Dorit TITLE OF INDENTION: WD-40 - Derived TITLE OF INVENTION: Thereof
	7153 MATTON:	NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS:
	APPLICANT: Greenwald, Iva APPLICANT: Hubbard, E. Jane	: ADDRESSEE: Dehlinger & Associates : STREET: P.O. Box 60850
	TITLE OF INVENTION: SEL-10 AND USES THEREOF NUMBER OF SEOURACES: 7	CITY: Palo Alto
	CORRESPONDENCE ADDRESS: ADDRESSEP. CONDERS:	COUNTRY: USA
	STREETS 195 Avenue of the Americas	COMPUTER READABLE FORM:
	STATE: New JOIN STATE: New York	COMPUTER: IN PLOTAD ALSO
		SOFTWARE: PATENTIN SISTEM: PC-DOS/MS-DO
	COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/190,802
	ttible DOS/MS-DOS	FILING DATE: 01-FEB-1994 CLASSIFICATION: 530
	SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:	; ATTORNEY/AGENT INFORMATION: ; NAME: Fabian, Gary R.
	APPLICATION NUMBER: US/08/899,578	E S
	ELLANG DATE: 24-002-199/ CLASSIFICATION: 435 AMMONINY AND TATION: 435	TION INFORMATIC
	ATTORNET/AGENT INFORMATION: NAME: White, John P.	; TELEFHONE: (412) 324-0860 ; TELEFAX: (415) 324-0960
	REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 0575/53200/JPW/AKC	; INFORMATION FOR SEQ ID NO: 30: ; SEQUENCE CHARACTERISTICS:
	TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400	; LENGTH: 517 amino acids ; TYPE: amino acid
н 	TELEFAX: (212) 278-0525 NFORMATION FOR SEQ ID NO: 6:	; TOPOLOGY: unknown ; MOLECULE TYPE: peptide
	SEQUENCE CHARACTERISTICS: LENGTH: 209 amino acids	HYPOTHETICAL: NO
!.	TTPE: Amino acid STRANDEDNESS: single	; ONLGINAL SOURCE:   : TNDIVIDHAL ISOLATE: BETA TRCP.

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-SU	US-08-190-802A-30	REFERENCE/DOCKET NUMBER: 8600-0139 - TELECOMMUNICATION INFORMATION: TELECOMMUNECATION:
OMĬ	Query Match 19.8%; Score 623; DB 1; Length 517; Best Local Similarity 31.1%; Pred. No. 2.6e-54; Matches 161; Conservative 89; Mismatches 214; Indels 54; Gaps 13;	(415) 32 R SEQ II RACTERIS
QY Db	<pre>60 VRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITSVQPP 113</pre>	; LENGTH: 7/9 amino acids ; TYPE: amino acid ; TOPOLOGY: unknown · MOLFOTLF TVPE' - rootein
oy Bb	LIDSCEPTOVKHMOVIEPOFORDFISLLPKE 1                            LISRMCHYOHGHINTYLKPMLORDFITALPARGLDH 1	HYPOTHERICAL: NO ANTI-SENSE: NO : ANTI-SENSE: NO : ORIGINAL SOURCE: : INDIVIDUAL ISOLATE: CDC4 / CDC20 protei
QY Db	<pre>170 LALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRR 221 1 11111 1 1 1 1 1 1 1 1 1 1 1 1 1 1</pre>	19.78: S
oy Db	GHDDHVI 26 : :	Best Loc Matches
γο d	TCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK 32 11: 1111 11:1:1 1:1:1 1:1:1 1:1:1 1:1:2 YCLQYDDKIVSGRDNTTRMKTLFKKNVTLFFKRVUMGHTGSVICTAVDBVTTTGS-DSTVD 20	13 LIDLIDCHTUCKNUNDVIELUCK     : : : : : : : : : : : : : : : : : :
vo da	VWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVMDIETGQCLHVLMGHV 3   :    ::      ::	RIFERSTRACTOR AND A CONTRACTOR AND AND A CONTRACTOR AND A
oy da	4 4	303 TGGVWS-SOMRDN
QV Dp	444 SIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQ 494 :  :  :	422 358
Oy Db		482 TGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTP 482 TGSRDNTLHVWKLPKESSVPDHGEEHDYPLVFHTP 395 RVVSGAVDFMVKVWDPETETCLHTLQGHTNRVYSL 1   :   :   :
ലഗ	RESULT 4 US-08-190-802A-32 ; Sequence 32, Application US/08190802A ; Patent No. 5519003 ; GENERAL INFORMATION ; ; APPLICANT: MACHIV-PASED, Daria	542 451 600
	Ron, Dorit VENTION: WD-40 - D VENTION: Thereof	DD 659 -ANDYSRKFSYHHTNLSALTTEVVSDNLVSGSEN-Q
	NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS: ASSOCIATES ADDRESSE: Dehlinger & Associates STREET: P.O. Box 60850 CTTVV: Delo Alto	QY 551 GGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDF 58 :1 : 1   1   :: 1 : 1   1 Db 714 -DQIWSVNFKGKTLVAAV-EKDGQSFLEILDF 74
		RESULT 5 US-08-283-917-3 ; Sequence 3, Application US/08283917 ; Patent No. 5849557
	MELLUW TIFE: FLOPPY disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRNT APPLICATION NUMBER: US/08/190, 802A APPLICATION NUMBER: US/08/190, 802A FILING DATE: 01-FEB-1994 CLASSIFICATION: 530 ATTORNEY/AGENT INFORMATION: NAME: Fabian, Gary R. REGISTRATION NUMBER: 33,875	GENERAL INFORMATION: APPLICANT: ADACHL, HIDEKI APPLICANT: TSUJIMOTO, MASAFUMI APPLICANT: INOUE, KEIZO APPLICANT: INOUE, KEIZO TTILE OF INVENTION: OXIDIZED PHOPHOLIPID I TITLE OF INVENTION: OXIDIZED PHOPHOLIPID I TITLE OF INVENTION: AND GENE THEREOF NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS: 31 ADDRESSEE: OBLOW, SPIVAK, MCCLELLAND, MJ ADDRESSEE: NEUSTADY, P.C.

<pre>sporecc: chakarTEFIFTCS: TYPE: mailon acids TYPE: mailo</pre>	
TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENZYME WINNER OF EFORMENDES. 340 GENE THEREOF	
NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS:	
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & ADDRESSER: NEUSTADT.P.C.	
AUDRESSEE: NEUSTAUT, P.C.	

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; Patent No. 5880272

: 1755 S. Jefferson Davis Highway, Suite 400 Arlington MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/283,917 PTLING DATE: 03-AUG-1994 CLASSIFCATION NUMBER: US/08/283,917 PRIOR APPLICATION DATA: 34 PRIOR APPLICATION DATA: 303-406-1993 APPLICATION NUMBER: JP 209943/1993 ATTORNEY/AGENT INFORMATION: NAME: Oblon, NO. 5849557man F. REGISTERANCION NUMBER: 2292-030-0 TELECOMMUNICATION INFORMATION: TELEPHONE: (703) 413-3000 TELEFAX: (703) 413-2220 TELEX: 248855 OPAT UR INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 409 amino acids TYPE: amino acid STRANDEDNESS: unknown COUNTRY: U.S.A. ZIP: 22202 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy di TOPOLOGY: unknown MOLECULE TYPE: peptide ORIGINAL SOURCE: Bos taurus STATE: Virginia COUNTRY: U.S.A. LENGTH: STREET: Query Match

10; 529 263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319 1 : :!! !:!! !:!! !! !! !!! !! !! !! ! ! :: !
108 SPVTRVIFHPVFSVMVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASC 167 228 TFTGHREWVRWVRPNQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPES 287 --DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD 473 288 SYSSISEATGSETKKSGKPGPFLLSGSRDKTIKMWDVSTGMCLMTLVGHDNWVRGVLFHS 347 -----VLKGHD 262 320 STDRTLKVWNAETGECIHTLYGHTSTVRCMHL--HEKRVVSGSRDATLRVWDIETGQCLH 377 378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDFETETCLHTLQGHTNRVYSLQF---- 431 Gaps 474 -- NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKN-- FVITSSDDGTVK 60; 14.0%; Score 439; DB 2; Length 409; 30.1%; Pred. No. 7.2e-36; tive 62; Mismatches 133; Indels 227 GFIHSPWKSAYIRQHRI------DTNWRRGELKSPK-RESULT 6 \_US-08-961-716-3 ; Sequence 3, Application US/08961716 Best Local Similarity 30.1 Matches 110; Conservative 1: : 405 VWECR 409 530 LWDLK 534 ; ORGANISM: US-08-283-917-3 432 đ qq q δ ą  $\mathcal{S}$ q S 5 S Qγ qq ò ą

227 GFIHSPWKSAYIRQHRI-----VLKGHD 262 1 : :|| :| |:|| || || || || || :| :: |
108 SPVTRVIFHPVFSVMVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASC 167 48 GLLEKKWTSVIRLOKKVMELESKLNEAKEEFTSGGPLGOKRDPKEWIPRPPEKYALSGHR 107 60; Gaps 14.0%; Score 439; DB 2; Length 409; 30.1%; Pred. No. 7.2e-36; tive 62; Mismatches 133; Indels APPLICANT: ADACHI, HIDEKI APPLICANT: TSUJIMOTO, MASAFUMI APPLICANT: INOUE, KEIZO APPLICANT: ARAI, HIROYUKI APPLICANT: ARAI, HIROYUKI TTLE OF INVENTION: AND GENE THEREOF TITLE OF INVENTION: AND GENE THEREOF NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & ADDRESSEE: NOLON, SPIVAK, MCCLELLAND, WAIER & STREET: 1755 S. Jefferson Davis Highway, Suite 400 OPERATING SYSTEM: PC-DOS/MS-DOS OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 APPLICATION DATA: APPLICATION DATA: US/08/961,716 PRIOR APPLICATION PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/283,917 FILING DATE: 03-AUG-1994 APPLICATION NUMBER: UP 209943/1993 FILING DATE: 03-AUG-1993 ATTORNEY/AGENT INFORMATION: NAME: 0blon, NO. 5880272man F. REGISTRATION NUBER: 24,618 REGISTRATION NOBER: 24,618 REGISTRATION NUBER: 24,618 REGISTRATION NOBER: 2292-030-0 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELEPHONE: 7(703) 413-3000 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible TELEFANONE: (703) 413-3000 TELEFAX: (703) 413-220 TELEEX: 24855 OPT UR TELEX: 248855 OPT UR INFORMATION FOR SED ID NO: 3: SEQUENCE CHARACTERISTICS: 409 amino acids Query Match 14.09 Best Local Similarity 30.19 Matches 110; Conservative unknown MOLECULE TYPE: peptide ORIGINAL SOURCE: ; ORGANISM: Bos taurus US-08-961-716-3 TOPOLOGY: unknown TYPE: amino acid STRANDEDNESS: un CITY: Arlington STATE: Virginia STATE: Virginia COUNTRY: U.S.A. GENERAL INFORMATION: FILING DATE: CLASSIFICATION: 22202 LENGTH:

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263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319 δ

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320 STDRTLKVWNAETGECIHTLYGHTSTVRCMHL - - HEKRVVSGSRDATLRVWDIETGQCLH 377 δ

qq

378 VLMGHVAAVRCVQ - - YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF - - - - 431 δ

q

---DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD 473 432 ð

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<pre>Db 288 SYSSISEATGSETKKSGKPGFFLLSGSRDKTIKMWDVSTGMCLMTLVGHDNWVRGVLFHS 347 Qy 474NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVK 529</pre>	169
Db 348 GGKFILSCADDKTLRVWDYKNKRCMKTLNAHEHEVTSLDFHKTAPYVVTGSVDQTVK 404 Ov 530 IMDIK 534	QY 378 VLMGHVAAVRCVQYDGRRVVSGAYDFWKVWDFETETCLHTLQGHTNRVYSLQF 431 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	Qy       432      DG1HVVSGSLDTSIRVMDVETGNCIHTLFGHQSLTSGMELKD       473         Di       289       SYSSISEATGKSGFFLLSGSENKTIKMMDVSTCMCIMTLVGHDNAVRGVLFHS       348
EESULT 7	474 NILVSGNADSTVKIMDIKTGQCLQTLQGPNKHQSAVTCLQFNKN FVITSSDDGTVK
05-06-203-91/9 5 Sequence 9, Application US/08283917 • Datant No. 5840557	21 21 21 21 21 21 21 21 21 21 21 21 21 2
GENERAL INFORMATION: GENERAL INFORMATION:	QY 530 LWDLK 534
APFLICANT: ADACHI, HIDEKI APPLICANT: TSUJIMOTO, MASAFUMI APPLICANT: INDIF KETA	:  : : 406 VWECR
APPLICANT: ARAL, HIROYUKI TITLE OF INVENTION: OXIDIZED PHOPHOLIPID DEGRADING ENXYME	«
TITLE OF INVENTION: AND GENE THEREOF NUMBER OF SEQUENCES: 31	US-08-961-716-9 : Sequence 9. Application US/08961716
CORRESPONDENCE ADDRESS: ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &	Fractant No. 5880272 GENERAL THEORANDITON:
TADT,P.C. Jefferson Davis Highwav. Sui	PPPLICANT: ADACHI, HIDEKI APPLICANT: ADACHI, HIDEKI ADDITIONUT: ADACHI, ULEKI
	I NOUE, I
	; APPLICANT: ARAI, HIROYUKI ; TITLE OF INVENTION: OXIDIZED PHOPHOLIFID DEGRADING ENZYME
COMPUTER READABLE FORM:	: 31 GENE
MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible	; CORRESPONDENCE ADDRESS; ; ADDRESSEE: OBLON. SPIVAK, MCCLELLAND. MATER &
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.25	NEUSTAD
CURRENT APPLICATION DATA: ADDITCATION NUMBED IIS /08 /283 017	Arlington
FILING DATE: 03-AUG-1994 CLASSIFICATION: 436	3 E
PRIOR APPLICATION DATA:	- H
APPLICATION NUMBER: JP 209943/1993 FILING DATE: 03-AUG-1993	<pre>&gt; MEDIUM TYPE: Floppy disk &gt; COMPUTER: IBM PC compatible</pre>
ATTORNEY/AGENT INFORMATION: NAME: Oblon, No. 5849557man F.	COFERATING SYSTEM: PC-DOS/MS-DOS COFFWAABF: DatantIn Palaace #1 0 Vareion #1 25
REGISTRATION NUMBER: 24,618 REFERENCE/DOCKET MIMBER: 2392-030-0	ATA:
TION INFORMATIC	FILING DATE: US/U8/961,716
TELEPHONE: (/U3) 413-3000 Telepax: (703) 413-2220	; CLASSIFICATION: ; PRIOR APPLICATION DATA:
TELEX: 248855 OPAT UR INFORMATION FOR SEO ID NO: 9:	; APPLICATION NUMBER: US 08/283,917 · ETITED DAPE: 03-ATC-1004
·· 7	ž
mino acid	FILLING DATE: U3-AUG-1993 ATTORNEY/AGENT INFORMATION:
TYPI	; NAME: Oblon, NO. 5800272man F. ; REGISTRATION NUMBER: 24,618
US-08-283-917-9	REFERENCE/DOCKET NUMBER: 2292-030-0 TELECOMMUNICATION INFORMATION:
14.0%;	; TELEPHONE: (703) 413-3000 ; TELEFAX: (703) 413-2220
Similarity 30.1%; Pred. No. 7.2e-36; 0; Conservative 62; Mismatches 133;	TELEX: 248855 OPAT UR INFORMATION FOR SEO ID NO: 9:
DTNWRRGELKSPKVLKGHD 262	SEQUENCE CHARACTERISTICS:
:         : DD 49 GLLEKKWTSVIRLQKKVMELESKLNEAKEEFTSGGPLGQKRDPKEWIPPEKYALSGHR 108	; TYPE: amino acid ; TOPOLOGY: linear
QY 263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISG 319	MOLECULE TYPE: protein US-08-961-716-9
Db 109 SPVTRVIFHPVFSVMVSASEDATIKVMDYETGDFERTLKGHTDSVQDISFDHSGKLLASC 168	14 0%, Score 430
QY 320 STDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLH 377	Local Similarity 30.18; Pred. No. 7.2e-36;

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<ul> <li>27) GFIRSPAKGNITAQUAT: DOINT</li></ul>
<ul> <li>49 Litekurtylrationalisest.NBAREESK.NBAREESFIGEPLGGENERPERVALGENER 49 Litekurtylrationalisest.NBAREDSK.NBAREDSK.NBAREDSK.JAGG 40 SPTRVFIHYPSYM9ASAEDNTLKWADYCGREEPERLAGHDSYGOLEFUBSKLJAGG 40 SPTRVFIHYPSYM9ASAEDNTLKWADYCGREEPERLAGHDSYGOLEFUBSKLJAGG 40 SDAPTIKLMANETGECTHTVGHTSTWAGNHL-HERKRWOSGSRDATLAWDDEFGOCLLI 16 SDAPTIKLMANETGECTHTVGHTSTWAGNHL-HERKRWOSGSRDATLAWDDEFGOCLLI 40 SDAPTIKLMANETGECTHTVGHTSTWAGNHL-HERKRWOSGSRDATLAWDDEFGOCLLI 41 STATICLOFCONRIVOSGSLDSTRWWOMTRECKAELREIENENVECISAADSE 42 STATICLOFCONRIVESCONCTLASCSNOGTVRWWWATKECKAELREIENENVECISAADSE 43 STATICLOFCONTLASCSNOGTVRWWWATKECKAELREIENENVECISAADSE 43 STATICLOFCONTLASCSNOGTVRWWWATKECKAELREIENENVECISAADSE 43 STATICLOFCONTLASCSNOGTVRWWWATKECKAELREIENENVECISAADSE 44 ALLINGSANDSTFIKKGKREPELLSGSRDKTIKMODYSTGACLATLVGIDMWRGVLEHS 44 ALLINGSANDSTFIKKGKREPELLSGSRDKTIKMODYSTGACLATLVGIDMWRGVLEHS 44 ALLINGSANDSTFIKKGKREPELLSGSRDKTIKMODYSTGACLATLVGIDMWRGVLEHS 44 ALLINGSANDSTFIKKGKREPELLSGSRDKTIKMODYSTGACLATLVGIDMWRGVLEHS 44 ALLINGSANDSTFIKKGKREPELLSGSRDKTIKMODYSTGACLATLVGIDMWRGVLEHS 45 GKRELLSCADDKTLRWMDYKKKGKRELMANEHFVISLDFIKTAPTVVTGSVDOTW 46 WECK 4.10 46 WECK 4.10 46 WECK 4.10 46 WECK 4.10 46 WECK 4.10 46 WECK 4.10 46 WECK 1.10 46 WECK 4.10 46 WECK 1.10 46 WECK 2.10 46 WECK 2.10 46 WECK 2.10 46 WECK 2.10 47 ALLOSSTFIKSCONTELLSSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSVDOTW 47 ALLOSSTFIKSCONTELLSSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSVDOTW 46 WECK 2.10 46 WECK 2.10 46 WECK 4.10 46 WECK 2.10 47 ALLOSSTFIKSCONTELLSSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSVDOT 47 ALLOSSTFIKSCONTELLSSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSVDOTV 47 ALLOSSTFIKSCONTELLSSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSVDOTV 47 ALLOSSTFIKSCONTELLSSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSVDOTV 47 ALLOSSTFIKSCONTELLSSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSVDOTV 47 ALLOSSTFIKSCONTELLSSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSVDOTV 47 ALLOSSTFIKSCONTELLSSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSVDOTV 47 ALLOSSTFIKSCONTERSSNDGTVRLMANEHFVISLDFIKTAPTWYTGSNDGTVRL</li></ul>
<pre>7 35 DHVTTCL-OFCGNRTVSGSDDNTLKWASNTGNCLRTLVGHTGCWSGONBONIIISG 7 320 STDRTLKWMARTGECHTTKVGHTKWONDEFECLAGGHTNGVOJSPOHSGKLIAG 7 320 STDRTLKWMARTGECHTTKVGHTGHNGNOJSPOHSGNSTLAGGHTNGVOJSPOHSGKLIAG 7 320 STDRTLKWMARTGECHTTKVGHTGHNGGNTVAGGNGTGNSGSDATLAMDEFECLATLGGHTSVDJSCO 7 378 VLMGHVANYCVOYDGRKVSGAVDEPWKWNDEFETCLATLGGHTNMGVOJSCO 8 378 VLMGHVANYCVOYDGRKVSGAVDEPWKWNDEFETCLATLGGHTNGGOST 8 42DGHTVSGSLDGTVAMGVGTLAGGGTNAGGVDTV 8 42DGHTVSGSLDGTVAMGVGTLAGGGTNAGGVDTV 8 42DGHTVSGSLDGTVAMGVGTLAGGGTNAGVDIN 9 42DGHTVSGSLDGTVAGGTLAGGSDQTVWWVTFCCALFLUGHTNGTON 9 43DGHTVSGSLDGTVAGGTLAGGSDQTVW 9 530 LMDLX 54 14</pre>
<pre>109 SPTRVITHUVESVASSEDATIKWOPTEGDERTLEGHTSODISEDASCKLIASC 30 STORTLAWMARTGGCTUTAGETSTWOCHL-IEREKTVSSSEDATIKWMEVOCCVV 310 VLMGUNAPTGGCTUTAGETSTWOCHL-IEREKTVSSSEARTLRWEVOCCSWAPS 311    1     1     1     1     1     1     1     1     1  229 TETGHREWTEWVECV-PORRVVSCAPTERTCLIFTLGGFTRAVVSCIP 412</pre>
<pre>2 32 STDFTLAWMARTGGGTTLAGTSTWOCHLL-IERAWYSGSERAMTLAWDITCGGUT 3 20 STDFTLAWMARTGGGTECTETWHGHDINYSSANTWORDHITYSASRATTKAMEYGTGYCW 3 30 VLAGTAVAVCYO-YDGRAWYGAWYDDFONTITYGAGSLFTSTMAEYGGTSMESE 2 23 TFTGARRAWYBAWYEPNOGGTLLASCSNOGTWAWWAATECKAELREBHENVECTSMESE 4 32</pre>
<pre>b 169 SADWFIKLWOFOCPECIFFYNGGHDHWYSSYAINPNCDHIYSASNAFTKWWENGOFYCYW 7 378 VLMGHNANREVQYCCRENVSGAUDENWYWUDDEFFCLHTLOGHTNENVSLOF 2 239 TFFGHREWNENVOCFLIASCSNOGTVRWWUNTRECKALERBENVECISARES 7 432</pre>
<pre>y 378 VLAGHIANNEYQYOTERVYSGAYDEWWYWDDEFFICALIFLGGHTRRWYSLOF</pre>
<pre>2 29 TFTCHREWNWWFRWOhTLANCSNDGTViNUWATKECKALEHEINVECSIABE 29 SYSSISBATGSETKKSGRPEPERLASSNDGTVINUWATKECKALEHEINVECSIABE 412NILVSGNDSTVKTWDIKTGGCLGTLAGGSNDGTVW 414NILVSGNDSTVKTWDIKTGGCLGTLAGGSNATLAMWDYSTGKLATV 413NILVSGNDSTVKTWDIKTGGCLGTLAGGNNHIGSAVTCLOFNKNFVITSSDDGTVK 414NILVSGNDSTLKWDIKTRGCLGTLAGGNNHIGSAVTCLOFNKNFVITSSDDGTVK 414NILVSGNDSTLKWDIKTRGCLGTLAGGNNHIGSAVTCLOFNKNFVITSSDDGTVK 414NILVSGNDSTLKWDIKTRGCLGTLAGGNNHIGSAVTCLOFNKNFVITSSDDGTVK 414NILVSGNDSTLKWDIKTRGCLGTLAGGNNHIGSAVTCLOFNKNFVITSSDDGTVK 416</pre>
<pre>4 43</pre>
<pre>2 29 SYSSISEATCSETKKSGKFÖRPLLSöSENÖKTIKNÄDVSTÖMCIMTIVGIDNWURGVLEHS 7 47NILVSGNADSTVKIMDIKTGGCLGTLGGFNKHGSAYTCLQFNKH-FVITSSDDGTVK 3 99 GGKTIIJ    1::1    1::1    1::1    1:1] 3 91 GGKTIZADDTTLRWUDTKNKGKMTLNAHEHFVYSLDFHKTAPTVTGSVDGTW 7 530 LMDLK 534 406 WBECR 410 2.08-190-8024-51 Sedel 190-8024-51 Sedel 190-8024 TITLE 0F INVENTION: WD-40 - Derived Peptides and Uses TITLE 0F INVENTION: WD-40 - Derived Peptides and Uses CONTERPRIJON: WD-40 - Derived Peptides and Uses TITLE 0F INVENTION: WD-40 - Derived Peptides and Uses TITLE 0F INVENTION: WD-40 - Derived Peptides and Uses CONTERPRIJON: WD-40 - Derived Peptides and Uses TITLE 0F INVENTION: WD-40 - DERIVED CONTERPRIJON: DORES: 265 CONTERPRIJON: DORES: Dellinger &amp; Associates CONTERPRIJON: DORES: Dellinger &amp; Associates CONTERPRIJON: WD-40 - DERIVED CONTERPRIJON: MD-41 - DORES: CONTERPRIJON: DORES: DELLINE CONTERPRIJON: DORES: DELLINE TITLE 0F INVENTION DATA: MME: Pablan. GSTO ATTORNER: DELLINE DELECTION DATA: MME: Pablan. GSTO ATTORNER: PART INCOMDAN: MME: Pablan. GSTO ATTORNER: PART INCOMDAN: MME: Pablan. GSTO ATTORNER: PART INCOMDAN: MME: Pablan. GSTO ATTORNER: PART INCOMDAN: MME: PABLANCHI: AND AND TELERONUNICATION NETARIANCES MME: PABLANCHI AND AND MME: PABLANCHI AND</pre>
<pre>Y 414NILVSGANDSTWYINDIKTGOCICUTCOENKNOSSWYTCLOFNKN - FYITSEDDGTWX Y 330 LWDLK 534 Y 530 LWDLK 534 A 66 WWECK 410 A 66 WWECK 410 A 66 WWECK 410 A 66 WWECK 410 B 406 WWECK 410 A 60 WWECK 410 B 406 WWECK 410 B 400 D 410 B 400 D 410 B 400 D 410 B 41 B 410 B 41 B 41</pre>
<pre>y 50 LWDLK 534 i)::</pre>
<pre>b 406 WWECR 410 b 406 WWECR 410 ESULT 9 ESULT 9 Sequence 51, Application US/08190802A Petent No. 5519003 RELETANT: MOCHLY-ROSEN, Daria APPLICANT: MOCHLY-ROSEN CORRESSIES Dehlinger &amp; Associates CORRESSONDERCE ADDRESS: ADDRESSEE: Dehlinger &amp; Associates CORRESSONDERCE ADDRESS ADDRESSEE: Dehlinger &amp; Associates CORRESTATA COUNTR: Palo Alto SOFTARTS APPLICATION NUMBER: US/08/190, 802A CLASSTRATION NUMBER: US/08/190, 802A ATTIKE APPLICATION NUMBER: US/08/190, 802A TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELERONS: (415) 324-0960 INFORMATION FOR SEC ID NO: 51: SEQUENCE CARACTERISTICS: LENCTH: 409 amino acid TOPOLGGT: UNADOWN MOLECULE TYPE: PLOCEN MOLECULE TYPE: PLOCEN MOLECU</pre>
<pre>ESUUT 9 5-08-190-802A-51 Sequence 51, Appl.cation US/08190802A Patent No. 5519003 GENERAL INFORMATION: APPLICANT: Moon. Dorit TITLE OF INVENTION: WD-40 - Derived Peptides and Use TITLE OF INVENTION: WD-40 - Derived Peptides and Use TITLE OF INVENTION: WD-40 - Derived Peptides and Use NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS: ADDRESSE: Denilinger &amp; Associates STREET: P.O. BOX 60850 CUNTRY: USA STREET: P.O. BOX 60850 CUNTRY: USA COUNTRY: USA STREET: P.O. BOX 60850 CONTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA COUNTRY: USA STREET P.O. BOX 60850 CONTRY: USA COUNTRY: USA</pre>

•• Đ	; INDIVIDUAL ISOLATE: LISI (human), F1g. 34 US-08-190-802A-51
	Query Match 13.5%; Score 424.5; DB 1; Length 409; Best Local Similarity 29.9%; Pred. No. 2.1e-34; Matches 109; Conservative 62; Mismatches 133; Indels 61; Gaps
δĒ	QY       227       GFIHSPWKSAYIRQHRIUTNWRRGELKSPKVLKGHD       262         I       I       I       I       1         DD       49       GLLEKKWTSVIRLQKKVMELESKLNEAKEEFTSGGPLGQKRDPKEMIPRPPEKYALSGHR       108
ο c	QY     263     DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISG     319       Db     100     summary matrix and an an an and an
ιó	100 JETINTER FLOWING SCHULLY GHTSTVRCHLEIGUE EN LEGEN
	169 SADMTIKLWDFOGFECIRTWHGHDHNVSSVAIMPNGDHIVSSSRDKTIKMWEVQTGYCVK
ο i	378 VLMGHVAVRCVOYDGRRVVSGAYDFMVKVWDFETETCLHTLOGHFNRVYSLOF
ΞÓ	Db 229 TFTGHREWVRNVRPNQDGTLIASCSNDQTVRVWVVTKECKAELREHEHVVECISWAPES 288 0v 432bdihvvSgsLDTSIRVWDVETGNCIHTL/GHOSLTSGMELKD 473
ā	<pre>1 ::!!! : ::!!! : ::!!! !: !! !! !: !! 289 SYSSISEATGSETKKSGKPGPFLLSGSRDKT-KMWDVSTGMCLMTLVGHDNWVRGVLFHS</pre>
à	QY 474NILVSGNADSTVKIMDIKTGDCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVK 529
ā	1:1     1:1:1     1:1:1     11     11       Db     348     GGKFILSCADDKTLRVWDYKNKRCMKTLNAHEHFVTSLDFHKTAPYVVTGSVDQTVK     404
õ	QY 530 LWDLK 534
ā	Db 405 VWECR 409
8.5.	RESULT 10 US-08-899-578-7 ; Sequence 7 , Application US/08899578
	a Arricant: Greenward, 1va APPLICANT: Hubbard, E. Jane TITLE OF INVENTION: SFL-10 AND USES THEREOF
	R OF SEQUENCES: 7 SPONDENCE ADDRESS:
•• ••	ADDRESSEE: Cooper & Dunham LLP STREET: 1185 Avenue of the Americas
•• ••	ew Yor New Yo
	COUNTRY: U.S.A. ZIP: 10036 COMPUTED BARAART FORM.
• •• •	TYPE:
	COMPUTER: LEM PC COMPATIDLE OPERATING SYSTEM: PC-DOS/MS-DOS COURTADED DEFACTIF DEJABLOSOS #1 20
	101200 710/ 7013100 71.
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	KEFERUCE/DUCKET NUMBER: U5/5/53ZUU/JFW/AKC TELECOMMUNICATION INFORMATION: meterducke. / /13 772-/14
	TELERANCE: (1.12) 2/8-0400 TELERAX: (2.12) 278-0555 TEREDAMANTON FOR SED TO NO. 7
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i:| :|: || || : :::: :|: || :::: 1| 67 YLLKWLDPQTLL----TCCLVSKQRNKVISACTEVWQTACKNLGWQIDDSVQDSLH---- 118 243 SGSADFAVKVWALSAGTCLNTLTGHTEWV-------TKVVLQKCKVKSLLH 286 117 QEWLK ----MFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKELAL 172 222 KVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSD 281 282 DNTLKVWSAVTGKCLRT - - LVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTL 339 340 YGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRR--VV 397 SGAYDFWVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIH 457 287 S--------PGDYILLS--ADKYEIKIWPIGREINCKCLKTL---SVSEDRSICLQ 329 173 YVLSFLEPKDLLQAAQTC-----RYWRILAEDNLLWREKCK-----EEGIDEPLHIKRR 221 185 QTHTCA - - AVKFDEQKLVTGSFDNTVACWEWSSGARTQHFRGHTGAVFSVDYSDELDILV 458 TLTGHQSLTSGMELKDNILVSGNADS-TVKIWDIK---TGQCLQTLQGPNKHQSAVTCLQ 12.0%; Score 376.5; DB 1; Length 422; 25.6%; Pred. No. 1.6e-29; cive 75; Mismatches 140; Indels 125; RESULT 12 US-08-190-802A-66 Sequence 66, Application US/08190802A Patent No. 5519003 CRIREAL INFORMATION APPLICANT: Mochly Rosen, Daria APPLICANT: Mochly Rosen, Daria APPLICANT: Ron, Dorit TITLE OF INVENTION: MD-40 - Derived Peptides and Uses TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS: ADDRESSEE: Dellinger & Associates STREET: P.O. BOX 60850 STREET: P.O. BOX 60850 CUPPER READABLE FORM: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible SOFTWARE: Patentin Release #1.0, Version #1.25 CURREWT APPLICATION DATA: APPLICATION NUMBER: US/08/190,802A FILING DATE: 01-FEB-1994 CLASSIFICATION: 530 330 PRLHFDGKYIVCSSALGLYQ-WDFASYDILRVIKTPE 365 514 ----FNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLE 546 ATTORNEY/AGENT INFORMATION: NAME: Fabian, Gary R. REGISTRATION NUMBER: 33,875 REGISTRATION NUMBER: 33,875 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: / INDIVIDUAL ISOLATE: MD6, Fig. 35 US-08-190-802A-52 Best Local Similarity 25.69 Matches 117; Conservative COUNTRY: USA ZIP: 94306-0850 USA Query Match 398 δ a q đ ą q q q q  $\delta$ οy δ δ δ 20 δ 10; 260 GHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWS-SQMRDNIIIS 318 319 GSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHE----KRVVSGSRDATLRVWDIETGQ 374 375 CLHVLMGHVAAVRCVQYDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQFDGI 434 93 -----GHMASVRTVSGHONIVVSGSYDNTLIVWD------GHTDRIYSTIYD-- 134 435 H----VVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDI 490 
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 HERKRCISASAMDTTIRIWD------GHTALVGLLRLSDKFLVSAAADGSIRGWDH
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 Gaps 1 111111 1:::1:1 :::1 1 GHMTSVITCLQFEDNYVITGADDKMIRVYD-------GHDGGVWALKYAHGGILVS 49 92 50 GSTDRTVRVWD-------GHNSTVRCLDIVEYKNIKYIVTSGRDNTLHVW------78; Length 212 Sequence 52, Application US/08190802A Patent No. 5519003 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Mochly-Rosen, Daria APPLICANT: Rosen, Daria 60; Indels COMPTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/190,802A FILING DATE: 01-FEB-1994 CLASSIFICATION: 530 ATTORNEY/AGENT INPORMATION: 13.0%; Score 410; DB 3; 34.9%; Pred. No. 2.1e-33; Local Similarity 34.9%; Pred. No. 2.1e-les 96; Conservative 41; Mismatches 491 KTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDD 525 184 HT ------NLSAITTFYVSDNILVSGSEN 206 8600-0139 NAME: FABLAN, GARY R. NAME: FABLAN, GARY R. REGISTRATION NUMBER: 33,875 REFERENCE/DOCKET NUMBER: 86( TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880 TELEPAX: (415) 324-0860 INFORMATION FOR SEQ ID NO: 52: SEQUENCE CHARACTERISTICS: : 422 amino acids amino acid single TOPOLOGY: unknown MOLECULE TYPE: protein HYPOTHETICAL: NO peptide linear ZIP: 94306-0850 ; TOPOLOGY: 11 ; MOLECULE TYPE: US-08-899-578-7 USA STRANDEDNESS: ANTI-SENSE: NO ORIGINAL SOURCE: US-08-190-802A-52 COUNTRY : Query Match Best Local S Matches 96; LENGTH: Ξ RESULT g δ qq 5 đ δ đ ò δ q

STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STRTE: California COUNTRY: USA COUNTRY: USA ZIP: 94111-4187 CONDUTER READBLE FORM: MEDIUM TYPE: FLOPPY disk COMPUTER: TBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PLAENTIN RELEASE #110, VERSION #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/180.582 FITING DATE: 03-134.100, VERSION #1.25 CURRENT APPLICATION DATA:		Query Match10.6%; Score 332; DB 1; Length 704;Best Local Similarity29.0%; Pred. No. 1.22-24;Matches88; Conservative61; Mismatches126; Indels28; Gaps13;Oy257 VLKGHDDHVITCLQFC-GNRIVSGSDNTLKWSAVTGKCLFTLVGHTGGWSSQMRDN314Oy257 VLKGHDDHVITCLQFC-GNRIVSGSDNTLKWSAVTGKCLFTLVGHTGGWSSQMRDN314Oy373 VLNSHQGVTCAEISDSTMLACGFGDSSVRIMSLTPAK-LRFLKDABSLRE-422Oy315 IIISGSTPTLKWMAFTGGCIFTLYGHTSTV-RCMHLHERK-VVSGSRDATLRVWDIET373Oy315 IIISGSTPTLKWMAFTGGCIFTLYGHTGFVRSKLMSLLTPAK-LRFLKDABSLRE-422Oy313 GOCLHVLMGHVANCVQY-DGRTVCMFTGFVRSKLMSLLTPAK-LRFLKDABSLRE-422Oy373 GOCLHVLMGHVANCVQY-DGRTVFKGAFDEMNLLLSCSEDSTIRLMSLLT481Oy373 GOCLHVLMGHVANCVQY-DGRTVFMKWWDFFFFCLHTLQGHTNRVSLL431F111111111111Db482 WSCVVTYRGHVYFPWWDYFFFVSCSYDKTARLMATDSNOALRVFVGHLSDVDCVQ541Oy431 FDGIHVVSGSLDFSIRWWVETGNCIHTLFGHQSLTSGMELK - DNILVSGNDSFVK486Db431 FDGIHVVSGSLDFSIRWWVETGNCIHTLFGHQSLTSGMELK - DNILVSGNDSFVK486Oy431 FDGIHVVSGSLDFSIRWWVETGNCIHTLFGHQSLTSGMELK - DNILVSGNDSFVK486Oy431 FDGIHVVSGSLDFSIRWWVETGNCIHTLFGHQSLTSGSDSSLSACGNLLAS-TGNCINSFVK486Oy431 FDGIHVVSGSLDFSIRWWVETGNCIHTLFGHQSLSSSSSSSLSNCGNLLAS-TGNCINSFVK486Oy431 FDGIHVVSGSLDFSIRWWUFGSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS	QY543 VTL 545Db659 ITV 661RESULT14US-08-646-715-5Sequence 5, Application US/08646715Sequence 5, ApplicationSequence 5, ApplicationSequence 5, ApplicationSequence 5, ApplicationSequence 5, ApplicationSequence 5, ApplicationAppLICANT: TimothyAppLICANT: Horey, TimothyAppLICANT: Tanese, NaokoAppLICANT: Wang, EdithAppLICANT: Weinzierl, Robert 0.J.
TELEFAX: (415) 324-0960 INFORMATION FOR SED ID NO: 66: SEQUENCE CHARACTERISTICS: LENGTH: 514 amino acids TYPE: amino acid TYPE: TYPE:	Query Match11.6%; Score 364.5; DB 1; Length 514;Best Local Similarity23.0%; Pred. No. 3.6e-28;Matches119; Conservative116; MismatchesQy155 EPOFORDFISLLPRELALYULSFLEPKDLLQAAQTCRYWRILAED199      ::::! : !   !:!!!     : !:::! : ! ! !:::! Db15 EPOFORDFISLLPRELALIVULSFLEPKDLLAAQTCRYWRILAED199      ::::! : ! ! ! !:::!!!Db15 EAQLARE-VAIIPKDLPNVSIKFQALDTGDNVGGALRVPGAISEKQLEELLNOLNGTSDD73OY200 NLLWREKCREEGIDEPLHIKRKVIKPGFHBPWKSAYIR239Db74 PVPYTFSCTIGGKKASDPVKTIDITONLYSSLIKPGYNSTEDOITLLYTPRAVEKK130OY240 QHRIDTNWRGELKSPKVLKGHDDHVITCLQFCGRRIVSGSDDNTLKTWSAVTGKCL296Db131 PVTRSSSAIAGHGS-TILCSAFAPHTSSRMVTGAGDNTRARIMDCDTOTPM179	<ul> <li>QY 297 RTLVGHTGGYWSSOMRDNIIIEGSTDRTLKVWNAETGECI-HTLYGHTSTVRCM 349</li> <li>Db HTLKGHTNWVLCVSWSPDGEVIATGSMDNTIRLWDPKSQCICGDALRGHSKWITSLSW 237</li> <li>QY 350HLEHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQTDGRRVV-SGAT 401</li> <li>Db 238 EPHLLVKPGSKPRLASSSKDGTIKIMDTVSRVCQYTMSGHTNSVSCVKWGGQGLLYSGSH 297</li> <li>QY 402 DFMVKWDPETE-TCLHTLQGHTNRVYSLQFDGIH</li></ul>	RESULT 13 US-08-18B-582-5 Sequence 5, Application US/08188582 Patent No. 5534410 CENERAL INPORMATION: APPLICANT: Tjian, Robert APPLICANT: Tjian, Robert APPLICANT: Ponlact, Brian D. APPLICANT: Hoey, Timothy APPLICANT: Hoey, Timothy APPLICANT: Hoey, Timothy APPLICANT: Hoey, Timothy APPLICANT: Mang, Edith APPLICANT: Wang, Edith APPLICANT: Mang, Edith APPLICANT: MARKON, MARKENS, MARKON, MERENS, MARKON, MERENSERE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT ADDRESSERE: FLERR, HOHBACH, TEST, ALBRITTON & HERBERT

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APPLICANT: RON, Dorit TITLE OF INVENTION: WD-40 - Derived Peptides and Uses TITLE OF INVENTION: Thereof NUMBER OF SEQUENCES: 265 CORRESPONDENCE ADDRESS: 265 CORRESPONDENCE ADDRESS: ADDRESSE: Dehlinger & Associates STERET: P.O. BON 60850 CITY: Palo Alto

Mochly-Rosen, Daria

APPLICANT :

COMPUTER: IBM PC FONDELIDIE COMPUTER: IBM PC FONDELIDIE OPERATING SYSTEM PC-DOS/MS-DOS SOFTWARE: PALENTIN RELEASE #1.0, VERSION #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/190,802A FILING DATE: 01-FEB-1994 CLASSIFICATION: 530

Floppy disk

COUNTRY: USA ZIP: 94306-0850 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

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STATE:

CLASSIFICATION: 530 ATTORNEY/AGENT INPORATION: NAME: Fablan, Gary R. REGISTRATION NUMBER: 33,875 REFERCE/DOFKET NUMBER: 9600-0139 TELEPHONE: (415) 324-0960 TELEPHONE: (415) 324-0960 INFORMATION FOR SED ID NO: 62: SEQUENCE CHARACTERISTICS:

704 amino acids

LENGTH:

TYPE:

MOLECULE TYPE: protein HVPOTHETICAL: NO

unknown amino acid

TOPOLOGY :

13; 257 VLKGHDDHVITCLQFC--GNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDN 314 1 1 1 1 1 1 2 1 2 1 1 2 1 1 2 2 373 YLLWEAGG- VTCAEISDDSTMLACGFGDSSVRIWSLTPAK-LRTLKD-----ADSLRE- 422 315 IIISGSTDRTLKVWNAETGECIHTLYGHTSTV-RCMHLHEKR-VVSGSRDATLRVWDIET 372 : | | ::: : :|| :| || | | | | | :: | |:|:|:|:| : | 481 423 -LDKESADINVRMLDDRSGEVTRSLMGHTGPVYRCAFAPEMNLLLSCSEDSTIRLWSLLT 481 373 GQCLHVLMGHVAAVRCVQY - - DGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQ 430 Gaps TATA-BINDING PROTEIN ASSOCIATED FACTORS, NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE 28; 10.6%; Score 332; DB 1; Length 704; 29.0%; Pred. No. 1.2e-24; Query Match 10.6%; Score 332; DB 1; Length 70 Best Local Similarity 29.0%; Pred. No. 1.2e-24; Matches 88; Conservative 61; Mismatches 126; Indels NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: 36 CORRESPONDENCE ADDRESS: ADDRESSEE: FEHR, HOHBACH, TEST, ALBRITTON & HERBERT STREET: 4 Embarcadero Center, Suite 3400 CITY: San Francisco STATE: California CONTRE: California 21P: 94111-4187 21P: 94111-4187 SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/646,715 FILING DATE: 09-MAY-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: US 08/188,582 FILING DATE: 28-JAN-1994 ATTING DATE: 28-JAN-1994 NAME: OSMAN, RICHAIA NAME: OSMAN, RICHAIA REGISTRAFION NUMBER: 36,627 REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION: TELEFONE: (415) 781-1989 TELEFAX: (415) 781-1989 TELEFAX: (415) 388-3249 TELEFAX: (415) 388-3249 TELEFAX: (415) 398-3249 TELEFAX: (415) 777299 TELEFAX: (415) 77729 SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPALIDLE OPERATING SYSTEM: PC-DOS/MS-DOS LENGTH: 704 amino acids TYPE: amino acid COMPUTER READABLE FORM: MEDIUM TYPE: Floppy ; MOLECULE TYPE: protein US-08-646-715-5 TITLE OF INVENTION: TITLE OF INVENTION: linear TOPOLOGY : TYPE: q q δ S ò

13; 541 542 602 IWDLSNGSLVTTLL---RHTSTVTTITFSRDGTVLAAAGLDNNLTLWPFHKVTEDYISNH 658 || | :|| : :|: : :|::::|| :| :|| : :|: 373 VLNSHQG--VTCAEISDDSTMLACGFGDSSVRIMS-LTPANVRTLKD------ADSLRE- 422 315 IIISGSTDRTLKVWNAETGECIHTLYGHTSTV-RCMHLHEKR-VVSGSRDATLRVWDIET 372 : | | ::: : : | :| | | | | | | :: | |:|::: : | 433 -LDKESADINVRMLDDRSGEVTRSLMGHTGPVYRCAFAPEMNLLLSCSEDSTIRLWSLLT 481 373 GQCLHVLMGHVAAVRCVQY -- DGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQ 430 F - - DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELK - - DNILVSGNADSTVK 486 257 VLKGHDDHVITCLQFC -- GNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDN 314 Gaps 487 IWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSD--DGTVKLWDLK--TGEFIRNL 28; 10.4%; Score 326; DB 1; Length 704; 28.7%; Pred. No. 4.7e-24; Live 63; Mismatches 125; Indels Query Match 10.4% Best Local Similarity 28.7% Matches 87; Conservative 543 VTL 545 ITV 661 629 431 q δ Q qq δ qq g qD q δ S 5

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F---DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELK--DNILVSGNADSTVK 486 

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 IWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSD--DGTVKLWDLK--TGEFIRNL 542 111: 1 : 1 : 1 : 1 : 1:: :: :: 1 : 111 1: 558
602 IWDLSNGSLVTTLL---RHTSTVTTITFSRDGTVLAAAGLDNNLTLWDFHKVTEDYISNH 658

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US-08-190-802A-62 ; Sequence 62, Application US/08190802A ; Patent No. 5519003 ; SENERAL INFORMATION:

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<pre>D 474 -IEGVWEIAADHLRLISGAHDGVVKVWEACECVHTLKNHSEPVTSVALGDCEVVS 527 Qy 522 SSDDGTVKLW 531 Qy 522 SSDGTVKLW 531 Db 528 GSEDGKIYLW 537 RESULT 3 S49932 MET30 protein - yeast (Saccharomyces cerevisiae) N;Alternate names: protein Y19905.02; protein Y1L046w C;Date: 28 Hav-1993 #secuence revision C;Date: 24 Hav-195 #review C;Date: 24 Hav-2010 C;Date: 2</pre>	1995 #text_cmange 994 B:g603997; PID:g76 Werjan, Y. 993 PID:g432494 WD repeat homology	Query Match20.7%; Score 650; DB 2; Length 640;Best Local Similarity20.7%; Score 650; DB 2; Length 640;Matches163; Conservative 114; Mismatches197; Indels 144; GapsMatches163; Conservative 114; Mismatches197; Indels 144; GapsOy7 PriunicLuPUDLKSAKEDLPHOTVMKIFSISIIA0GLPECRRMKRKLDHGSEVRSFSLG 66Db68PSSSPDLATNDSGTRVQDLEFKNFKTHURKLDHGSEVRSFSLG 66Oy67KKPCKUSEYTSTGLUPCSATPTFGDLRANGGGQRRRTSVOPFTGLOBHL 120Db108HTACYKODLKFTGULKANGOCGQRRRTSVOPFTGLOBHL 120Db108HTACYKODLKFTGULKANOVEDPOFORDERSLLANGGGQGRRRTSVOFFEE 179Oy51KKPCLURKLNDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVLISFLD 200Oy121KMPOSWGSPRKLIALDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVLISFLD 200Oy121KMPOSWGSPRKLIALDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVLISFLD 200Oy121KNPOSWGSPRKLIALDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVLISFLD 200Oy121KNPOSWGSPRKLIALDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVLISFLD 200Oy121KNPOSWGSPRKLIALDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVLISFLD 200Oy121KNPOSWGSPRKLIALDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVLISFLD 200Oy122KNPOSWGSPRKLIALLDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVERSKLIASTOy121KNPOSWGSPRKLIALLDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVERSKLIASTOy121KNPOSWGSPRKLIALLDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVERSKLIASTOy121KNPOSWGSPRKLIALLDELLD-SCEPTOVKHMOVIEPOFORDERSLLAVERSKLIASTD122SKVSNONTRRKLILLDELL-SCEPTOVKHMOVIEPOFORDERSLLAVERSKLIATD142SKVSNONTR
Qy436-VVSGSLDTSIRVWDV ETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIK491Db1	<pre>RESULT 2 T38922 T38932 probable sulfur metabolite control protein - fission yeast (Schizosaccharomyces pombe) C:Species: Schizosaccharomyces pombe C:Species: Schizosaccharomyces pombe C:Species: Schizosaccharomyces pombe C:Accession: T38932 R:Badcock, K.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A. A. Submitted to the EMBL Data Library, April 1997 A:Reaction in T38932 A:Accession: T38</pre>	<pre>KRKLDHGEVERSELGKKPCKVSEYTSTGLVPCSATPTTFGDLRAANGGGORRRTTSY 110 [1:1]</pre>

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q	437 FSCSDDTTIRMWDIRTNSCLKVFRGHVGQVQKIIPLTIKDVENLATDNTSDGSSPQDDPT 496	QY	166 LPKELALYVLSFLEPKDLLQAAQTCRYV
δλ	OPDG	qq	242 LPFSIVQSILLNLDIHSFLSCRLVSPTV
qq	497 MTDGADESDTPSNEQETVLDENIPYPTHLLSCGLDNTIKLMDVKTGKCIRTQFGHVEGVW 556	QY	222 KVIKPGFIHSPWKSAYIRQHRIC
oy Db	<pre>468 GMELKDNILVSGNADSTVKIMDIKTGOCLQTLQGPNKHQSAVTCLQ 513 57 DIAADNFRIISGSHDGSIKVWDLQSGKCMHTFNGRRLQRETOHTOTOSLGDKVAPIACVC 616</pre>	, da Q	302 NLNRPPFLHNDQISDDYFPEIFKRHFLA 270 OFCGNPTVSGSDDNTLKVWSAVTGKTLF
οy		a d	
qq	EIT IGDSECFSGDEFGCVKMY 634	QY	
RESULT	17. 4.	qq	<pre>418 IEKAKCTHIFRGHISIIRCLEILVPSRI</pre>
T435 F-bo N-A1	WD-repeat protein pop2 -	σλ	371ETGQCLHVLMG : : : : : : : : : : : : : : : : : : :
C; Sp C; Da	avariated names: Protectives factor sugly C:Species: Schlacsaccharomyces pombe C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text change 21-Jul-2000	a ç	478 TDPPYLPDNTNSIDRWEKNPYFVHTLIC 414 TCLHTLAGHTNRVVSLAFDGIH VVSC
C;AC R;WO	C;Accession: T43557; T38794; T43798 R;Wolf, D.A.; Jackson, P.K.	g q	
A; De A; Re	submitted to the EMBL Data Library, December 1997 A:Description: Fission yeast pop2 encodes a novel F-box/WD-repeat protein involved in th A:Reference number: 22276	QY	472 KDNILVSGNADSTVKIWDIKTGQCLQTI
A; Ac A; St	ession: T43557 tus: preliminary; translated from GB/EMBL/DDBJ	qa	598 FONRLISGSADSTIRIWDLNTGRPLMVI
A; Mo A; Re	ecule type: mRNA idues: 1-703 <wol></wol>	Qγ	532 DLKTGEFIRNLVTLESGGSGGVVWRIRA
A; Cr	ss references: EMBL:AF038867; PIDN:AAB95480.1 erimental source: strain h- 972	qq	654 DVRTGKLLERFLLTDLTKIWHVDF
R;Ge subm	sticenties. S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V. submitted to the EMBL Data Library, August 1996	RESULT	LT 5
A; Ke A; Ac A: St	erence number: Z21812 ession: T38794 tue: nralimiarv: translated from CB/FMB1/NNB1	T16607 hypoth	07 thetical protein K10B2.1 - Caenorh
A; MO	cus, presiminary, transforce from ub/Embb/DUBJ ecule type: DNA idines 1-703 acpris	C; Sp C; Da	C;Species: Caenorhabditis elegans C;Date: 20-Sep-1999 #sequence_revision
A; Cr	ss-references: EMBL:298602; PIDN:CAB11275.1; GSPDB:GN00066; SPDB:SPAC4D7.03 erimental source: strain 972h-: cosmid c4D7	C;AC R;Mi	cession: T100U/ ller, N. ited A the EMDI Data Tibrary TV
R, Ja Proc		A; De A; Re	submitted to the Embirance of C. eleg A;Description: The sequence of C. eleg A;Reference number: 218545
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A; Re A; Cru	idues: 1-703 <jal> ss:references: EMBL:AF064515; NID:g3293382; PIDN:AAC39496.1; PID:q3293383</jal>	A; EX C; Ge	A;CTOSS-TETETENCES: EMBL:U28/3U; NID:9 A;Experimental source: strain Bristol C;Genetics:
C;Ge A;Gel A;Mal	24D7.03	A;Ge A;In	A;Gene: CESP:K10B2.1 A;Introns: 78/3; 125/1; 183/2; 281/3;
C;Fu A;De	c;Function: A;Description: required to prevent spontaneous re-replication	Be Me	Query Match 20.3%; Scor Best Local Similarity 33.5%; Pred Watchor 154, Concornatino 00, 00,
n e n B e n	4%; Score 641; DB 2; Length 703; 3%; Pred. No. 1.7e-42;	oy	EKLLALDELIDSCEPTQVKHMMC
Qy Qy	-	qq	<pre>1    :  : :::  : : 83 WSEHEQLDFMDKIVHRLSHYQLGKVDNF</pre>
qq	VSYKCLDHSPPDSVPGDFSISLVPQRNFLYSHSSLPPKIIS	QY	
οy	46 CRRRMKRKLDHGSEVRSFSLGKKPCKVSEVTSTTGLVPCSATPTTFGDLRAANGQGQQRR 105	a D	
qq	145 IDRNNRIKLDNSISSNSDNFPPSPKVDTSNTVSPGSKPISEDLEDLNLQSIVQ- 197	60 E	ZIU EGIDEFLHIKKKVIKPGFIHSPWKSAY
oy Db	106 RITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISL 165         :   :   :   :   :   :   :   :	oy	265 VITCLOFCGNRIVSGSDDNTLKVWSAVT
		qq	260 GVYCLQYDDDKIVSCLRDNTIKIWDRKD

5 8 8	166 LPKELA    : 242 LPFSIV	LPKELALYVLSFLEPKDLLQAAQTCRYW-RILAEDNLLWREKCKEEGIDEPLHIKRR 221    : :   :   : LPFSIVQSILLNLDIHSFLSCRLVSPTWNRILDVHTSYWKHMFSLFGFQINENDWKYANP 301	1
λα ά	222 KVIKPG : :  302 NLNRPP	KVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCL 269 : :  :  :  ::   ::   ::   ::   : NLNRPPFLHNDQISDDYFPEIFKRHFLNRKRWLFPSIPPSHLSFPIHVPNFMITSL 357	6 ٢
λα 40	270 QFCGNR :  358 LLHKDR	QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWN 329 (11::1 1::1 1::11 LLHKDRIITTSGSGTIQIHNAITGVLEARLEGHKEGVWAVKIHENTLVSGSLDKTVRVWN 417	6
2 Q	330 AETGEC   :  418 IEKAKC	AETGECIHTLYGHTSTVRCMHL	
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5 q	532 DLKTGE  ::  : 654 DVRTGK	DLKTGEFIRNLVTLESGGSGGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDF 584  ::  : :   :  ::   ::  DVRTGKLLRFLLTDLTKIWHVDFDAMRCVAAVQRDDQAYLEVINF 698	
ABSULT 5 ABSULT 5 Species: Species: Species: Accession aubmitted Accession Acces	<pre>SULT 5 6607 6607 5607 500 clast protein K1 500 clast clast protein K1 500 clast clast protein K1 500 clast clast clast clast accession: T16607 500 clast clast clast clast cross-references: LUA Accession: T16607 500 clast clast clast accession: T16607 500 clast clast clast cross-references: EMB Accession: T16607 500 clast clast cross-references: EMB Accession: T16607 500 clast clast cross-references: EMB Accession: T1607 500 clast cross-references: EMB Accession: T1607 500 clast cross-references: EMB Accession: T1607 78/31 clast cross-references: EMB Accession: T1607 78/31 clast cross-references: EMB Accession: T1607 78/31 clast cross-references: EMB Accession: T1607 78/31 clast cross-references accession: T1607 78/31 clast accession: T1607 78/31 clast accession: T180 78/31 clast accession: T180 78/</pre>	<pre>0B2.1 - Caenorhabditis elegans is elegans quence_revision 20-Sep-1999 #text_change 20-Sep-1 ata Library, June 1995 ence of C. elegans cosmid K10B2. 545 Ence of C. elegans cosmid K10B2. 545 Ence of C. elegans cosmid K10B2. 545 Ence of C. elegans cosmid K10B3. 545 Ence of C. elegans cosmid K10B3. 533.5% 51/3; 5668/3 183/2; 281/3; 404/3; 551/3; 668/3 183/2; 281/3; 404/3; 551/3; 668/3 183/2; 281/3; 404/3; 551/3; 668/3 183/2; 281/3; 404/3; 551/3; 668/3 20.3%; Score 639.5; DB 2; Length 701; 33.5%; Pred. NO. 2.2.8-42; vative 80; Mismatches 167; Indels 59; Gap 10: 11/11/11/11/11/11/11/11/11/11/11/11/11/</pre>	999 .1; CESP:KIOB 41 85 12; 64 64 64
5 7 7	260 GVYCLQ	VITCLOFCGNRIVSGSDDNTLKVWSAVTGKCLKTLVGHTGGVWSDDRHDNILISGSTDKT 324 :    : ::      :  :     :	

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<pre>Db 416 TIRLWDIEGGACLRVLEGHEELVRCIRFDNKRIVSGAYDGKIKVWDLVAALDFRAPAGTL 475 Gy 495 CLOTLOGFNKHQSAVTCLOFNKRFVISSDBGTVKLWD 532 Db 476 CLAFTLVEHSGRVFRLGFDEFQUYSSHDDTLLIWD 510 RESULT 7 TH 45136 WD repeat protein popl [imported] - fission yeast (schizosaccharomyces pombe) C.Speciess Schizosaccharomyces pombe C.Speciess Schizosaccharomyces pombe A.Romonyces prediminary translated from GB/EMBL/DBJ A.Romonted to the PMBL bata Library, March 1998 A.Romonted to the PMBL bata Library A.Romossion: 1775 4000 A.Romossion: 1775 4000 A.Romos</pre>	Query Match19.7%; Score 620; DB 2; Length 775; Matches 153; Conservative 100; Mismatches 179; Indels 124; Gaps 16; Matches 153; Conservative 100; Mismatches 179; Indels 124; Gaps 15; Matches 153; Conservative 100; Mismatches 179; Indels 124; Gaps 15; D 237 SHIPSNHLSZOKNAVLKIAQLISSFERLEESVRQYLLFHLLSRCGKHAYONIHKILLPFF 296 CQ 159 ORFEILFREIZEVERDLAAACTCRYW RILLABDLLUM
<pre>Qy 335 LKVWANETGECIHTLYCHTSTVRCMMLHEKRVVSGSRDATLRVWDIETGGCLHVLMG 381</pre>	Query Match20.2%; Score 634.5; DB 2; Length 518; Best Local Similarity 31.1%; Pred. No. 3.6e-42; Matches 161; Conservative 90; Mismatches 214; Indels 53; Gaps 12; Matches 161; Conservative 90; Mismatches 214; Indels 53; Gaps 12; DQY60 VRSFSLGKKPCKVSERTSTGLVPCSAFPT TFCDLRANGQG00 RRITSVOPP 113 I MECFSCSLDPPTASEREDNRDEPPRITTERWILMOTILINGTSMILVPGRKLAMTY 60 DQY114 TGLOBMLKNPGSWSGPEKLLALDELIDSCEPTOVKHMOVIEDGRDFSLLPKE 169 DQY114 TGLOBMLKNPGSWSGPEKLLALDELIDSCEPTOVKHMOVIEDGRDFSLLPKE 169 DQY114 TGLOBMLKNPGSWSGPEKLLALDELIDSCEPTOVKHMOVEDGRDFSLLPKE 169 DQY114 TGLOBMLKNPGSWSGPEKLLALDELIDSCEPTOVKHMOVEDGRDFSLLPKE 169 DQY114 TGLOBMLKNPGSWSGPEKLLALDELIDSCEPTOVKHMOVEDGRDFSLLPKE 169 DQY114 TGLOBMLKNPGSWSGPEKLLALDELIDSCEPTOVKHMOVEDGRDFSLLPKE 169 DQY116 TGLOBMLKNFGSWSGPEKLLALDELIDSCEPTOVKHMOVEDGRDFSKLASHLVERGNPCKLQY117 LAULISFLERFNCHARAKILERNVENDELMARKLIERNVERDELIDH120QY118 TGLOBMLKNFGSKSGSSGNENLENERKKLIERNVERGLAEQY120 LANLLSKLENKSLCSABLVCKWMRLDOLFTISKMMCGALEQY121 IAENILSKLENSSLCSABLVCKWMRLDERKKVELERNVENGELASQY121 IAENILSKLENSSLCSABLVCKWMRLUEDGRMENTERGNEGAQY122 KVIKPGFTHSSMCRCHARKLIERNVENGELASQY123 KCLOPTOGKVENKRSLCSSDNTKKSCKSDNTKLRSSQY267 TCLOFCGNNTSGSDDNTLKWSSVCKCGNWRSCKSDNMRKLIERNVENGTHRQY267 TCLOFCGNNTSGSDDNTLKWSSVCKCGNSENNECGNULLISSESTERGYQY268 TCLOFCGNNTSGSDDNTLKNSSCKSDNTLKSSSSDNTLRQY267 TCLOFCGNNTSGSSDNTLKNSSCKSDNTLKSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSQY268 TCLOFCGNNTSGSSDNTKNTLUCGTGGCWSSSONANDMASATD

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Db       366      YNPKEVPQRTTLRGHMTSVITCLQFEDNYVITGADDKMIRVYDSINKKFLLQLSGH       421         Qy       303       TGGVWS-SQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVV       357         Qy       303       TGGVWS-SQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVV       357         1111       1::1111:111:111:111:111:111111:11111111	<ul> <li>395 RUNGATDERWENDEFFETCLHTLOGHTNEVYSLOFDGTH</li></ul>	Qy551 GGVWRIRASNTKLVCAVGSRNGTEETKLLVLDF 584.1<	Gene 102, 135-1397, 1995 Construction A:Title: A gene responsible for vegetative incompatibility in the fungus Podospora an A:Reference number: 218944; MUID:96009891 A:Accession: T18521 A:Accession: T18521 A:Accession: T18521 A:Accession: T18521 A:Accession: T18521 A:Accession: T18521 A:Accession: T18521 A:Accession: T18521 A:Accession: T18521 A:Accession: T1852 A:Accession: T1852 A:Accessi	Query Match18.5%Score 582.5; DB 2; Length 1356;Best Local Similarity28.9%; Pred. No. 1.8e-37;Matches 169; Conservative85; Mismatches 193; Indels 137; GapsQy113 PFGLOEWLKMFOSWSGPEKLLALDELIDSCEPFQVKH 14911<11<11<1590 PESLEELVKLGSFLITRERTVYFVHQSAKFLLGTASDKASNKASOEAFELVFPTGIED 649Qy150 MNQVIEPQCRDFISLLPKELALVVLSFLEPKDLLQAAQTCRYW193b550 VSYIIFWRSLNVMSQKLRRDIYCLMAPGFLIDNVRVPDPDPLATVRYSCIYWIDHLRDLVb650 VSYIIFWRSLNVMSQKLRRDIYCLMAPGFLIDNVRVPDPDPLATVRYSCIYWIDHLRDLV	QY       194      RILAEDNLLWREKCKEBGIDEPL-HIKRKF       222         Db       710       SSTSSKWVHLLQDDGDIHRFLTFKYLYWLEALSLLRALPEGINAIROLESLLGHTIRGRL       769         QY       223      VIKPGFIDTN       246         Db       770       IAIVRDGYRALSYRMITEKAPLQAYTSALVFAPTDSMIKKIFKKEEPGWISTISVVEAE       829         QY       223      VIKPGFILPN       246         770       IAIVRDGYRFALSYRMITEKAPLQAYTSALVFAPTDSMIKKIFFKKEEPGWISTISVVEAE       829         QY       247       WRRGELKSPKVIKGHDBHVIT-CLQFCGNRIVSGSDDNTLKVWSAVTGKCLFTLVGHTGG       305         QY       247       WRRGELKSPKVLKGHDBHVIT-CLQFCGNRIVSGSDDNTLKVWSAVTGKCLFTLVGHTGG       305         QY       306       VWSSQMRDHIISGSTDRTLKVWNAETGECIHTLYGHTSKTMPTASGTGTGTLEGHGGS       885         QY       306       VWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRMHLHEKRVVSGS       360         QY       306       VWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRMHLHEKRVVSGS       360
QY       497       QTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLMDLKTGEFIRNLVTLESGGSGGSVWR 556         Db       1:1       1:1       1:1       1:1         Db       695       DILKCPLGHIFFQHDESKVVSGS-HSTLQLMDIRSGKLVRDLLTDLDIIWQ 744         Qy       557       IRASNTKLVCAVGSRN 572         Qi       557       IRASNTKLVCAVGSRN 572         Db       745       VAYNENVCVAAVLRNN 760	RESULT 8 556345 556345 cell division control protein CDC4 - yeast (Saccharomyces cerevisiae) N:Alternate names: protein YEN09w C:Species: Saccharomyces cerevisiae C:Species: Saccharomyces cerevisiae C:Species: 02-Sep1995 #sequence_revision 12-Apr-1996 #text_change 26-May-2000 C:Accession: 556245; 5481310; A26867; 562304 C:Accession: 556245; 5481310; A26867; 562304 R:Murakami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Murakami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Murakami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Murakami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Murakami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Markami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Markami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Markami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Markami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Markami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Markami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu R:Markami, Y.; Naitou, M.; Haguara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu	A;Molecule type: DNA A;Residues: 1-779 <mur> A;Residues: 1-779 <mur> A;Residues: 1-779 <mur> A;Cross-references: EMBL:D50617; NID:9836685; PIDN:BAA09229.1; PID:d1009870; PID:9836745 A;Cross-references: EMBL:D50617; NID:936685; PIDN:BAA09229.1; PID:d1009870; PID:9836745 A;Cross-reference number: S48310 A;Reference number: S48310 A;Recension: S48310 A;Recension: S48310 A;Residues: 1-579 <chu> A;Residues: 1-579 <chu> A;Residues: 1-579 <chu> A;Residues: 1-579 <chu> A;CHOS: references: EMBL:246255; NID:9559925; PIDN:CAA86341.1; PID:9559926; MIPS:YFL009w B;Cross-references: EMBL:24525; NID:9559925; PIDN:CAA86341.1; PID:9559926; MIPS:YFL009w J. Mol. Biol. 195, 233-245, 1987</chu></chu></chu></chu></mur></mur></mur>		Φ	Query Match19.7%; Score 618.5; DB 2; Length 779;Best Local Similarity29.6%; Pred. No. 1.2e-40;Matches 152; Conservative 105; Mismatches 176; Indels 81; Gaps 16;Qy135 LDELIDSCEPTQVKHMMQVIEPQFORPFISLLFKELALYVLSFLEPKDLLQAQTCRYW-193Qy135 LDELIDSCEPTQVKHMMQVIEPQFORPFISLLFKELALYVLSFLEPKDLLQAAQTCRYW-193Qy135 LFFLUANUDRSELSDLGTLKKUKRDLTSLPFEISLKFFWLQFEDINSLGVSONNN 306Qy194 RILAEDNLLMREKCEBGIDEPLHIKRRVIKPGFTHSPWKSAYIRQHIDFINN 248Qy194 RILAEDNLLMREKCEBGIDEPLHIKRRVIKPGFTHSPWKSAYIRQHIDFINN 24811:11:12:11:13:11:14:11:15:11:16:11:17:11:18:11:19:11:19:11:19:11:10:11:11:11:11:11:11:11:11:11:11:11:11:11:11:11:11:11:12:11:13:11:14:11:15:11:16:11:17:11:17:11:18:11:19:11:19:11:19:11:19:11:11:11:11:11:12:11:13:11:14:11:15:11:16:11:17:11:18:<

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Db      :   :   :   :   :   :   :   :   :	<pre>T50211 WD-repeat protein [imported] - fission yeast (Schizosaccharomyces pombe) C;Species: Schizosaccharomyces pombe C;Species: Schizosaccharomyces pombe C;Accession: T50211 R;McDougall, R.C.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Murphy, L.; Jones, L.; submitted to the EMBL Data Library, January 2000 A;Reference number: 225046 A;Reference number: 225046 A;Re</pre>	Query Match17.0%; Score 533; DB 2; Length 506;Best Local Similarity25.0%; Pred. No. 3.5e-34;Matches 140; Conservative 91; Mismatches 204; Indels 108; Gaps 14;Qy55 DHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTFFGDLRAAGGGQGRRITS 109Db55 DHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTFFGDLRAAGGGQGRRITS 1091:111:	Qy170LALYULSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCREGGIDEPL216Db80VSLRVFSYLDQLDLCKCKLMSKRWKRLLEDPGIWKALYMOKGWFVNENVLNBFFEAMRRTH139Qy217HIKRRVIKP-GFIHSPWKSAYIRQHRIDTNWRRGE251140KFPQPRFENFLKQONIIGPYGTMFLPQOFIFDSNGRPLLNWSYLKEHAHLDSNWRHGRF199Qy252LKSPKVLKGHDDHVITCLOFCGNBIYSGSDDTLKVWSAYTGKCLRTVG301Qy252LKSPKVLKGHDDHVITCLOFCGNBIYSGSDDTLKVWSAYTGKCLRTVG301Qy200LVSTFNNPSIRFPADQPRATLDSVYCQYDDEINVSGSDDTLKVWSAYTGKCLRTVG301Qy302HTGGVWSSQM-FDNTLKVWNAETGECIHILYGHTSTVRCMHLHEKRVVSG359Qy302HTGGVWSSQM-FDNTLKVWNAETGECIHILYGHTSTVRCMHLHEKRVVSG359Qy303HTGGVWSSQM-FDNTLKVMNAETGECIHILYGHTSTVRCMHLHEKRVVSG359Qy360SRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAYDFWKWMDFETE413Qy360SRDHTARVWLDATSSASSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS
Db       B86       VWSVAFSPDRER-VASGSDDKTIKIWDAASGTCTQTLEGHGGRVQSVAFSPDGQRVASGS       944         Oy       361       RDATLRVWDIETGQCLHVLMGHVAAVRCVQY - DGRRVVSGAYDFWVKWUDETETCLHT       418         Db       945       DhTTKIWDAASGTCTQTLEGHGSSVLSVAFSPDGQRVASGSGDKTIKIWDTASGTCTQT       1004         Qy       419       LOGHTNRVYSLOF - DGIHVVSGSLDTSIRVWDVFSPDGQRVASGSGDKTIKIWDTASGTCTQT       1004         Qy       419       LOGHTNRVYSLOF - DGIHVVSGSLDTSIRVWDVFSPDGGRVASGSGDKTIKIWDTASGTCTQT       1004         Qy       419       LOGHTNRVYSLOF - DGIHVVSGSLDTSIRVWDVFSPDGGRVASGSGDKTIKIWDTASGTCTQTL       1004         Qy       419       LOGHTNRVYSLOF - DGIHVVSGSLDTSIRVWDVFSDGGRVASGSGDKTKIKIMDTASGTCTQTL       1004         Qy       419       LOGHTNRVYSLOF - DGIHVVSGSLDTSIRVWDVFSDGGRVASGSDDGTVKIS       1004         Qy       419       LOGHTNRVYSLOF - DGIHVVSGSLDTSIRVWDVFSDGGRVASGSDDGTVKIS       1062         Qy       1005       LEGHGGSVWSVAFSPDGQRVASGSDDGTVKISSDDGTVKIS       1062         Qy       1111       111	RESULT 10 T46660 Sulfur controller-2 protein [imported] - Neurospora crassa c;Species: Neurospora crassa c;Species: Neurospora crassa c;Species: Neurospora crassa c;Species: Neurospora crassa c;Species: Neurospora crassa c;Accession: T46660 c;Accession: T46660 s;Accession: T46660 s;Accession: T46660 A;Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes a A;Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes A;Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes A;Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes A;Title: The sulfur controller-2 negative regulatory gene of Neurospora crassa encodes A;Title: The sulfur controller-2 negative regulatory A;Title: The sulfur controller-2 nef	A; Introns: 75/3; 319/1; 354/1 C; Function: A: Description: negatively regulates sulfur structural gene expression A: Description: negatively regulates sulfur structural gene expression A: Note: scorot+ expression is dependent on CYS3 function and the binding of CYS3 to the A: Note: scorot+ expression is dependent on CYS3 function and the binding of CYS3 to the C; Superfamily: unassigned WD repeat proteins; WD repeat homology C; Superfamily: unassigned WD repeat proteins; WD repeat homology (c; Superfamily: unassigned	<ul> <li>Db 71 XIII SILL</li> <li>Db 71 XIII SILL</li> <li>CLERELALTYUSFLERADAOTCHYWRIAEDINLUWREKCKEBGIDEPL 216</li> <li>129 ALPVELAGVVLCYLDTVSLTKAQVSORMTLAEDINLUWREKCKEBGIDEPL 216</li> <li>129 ALPVELAGVVLCYLDTVSLTKAQVSORMTLADSDAVWYRMCEQHVNKCTKGWGLPL 188</li> <li>0y 217HIKRKVKRG</li> <li>217FIHSPWKSATIRQHIDTUMRRGELKSPKVLKGHDHVITCLQFCGNLPL 188</li> <li>0y 217FIHSPWKSATIRQHIDTUMRRGELKSPKVLKGHDHVITCLQFCGNR 275</li> <li>189 LERKLRNYTRQRQLAKGGPGGRYTELADSHDSODRSVNOHGKRPAAEAEEEDPIKKROC 248</li> <li>0y 228FIHSPWKSATIRQHIDTUMRRGELKSPKVLKGHDHVITTCLQFCGNR 275</li> <li>249 MAAAEASKAVTQPKTRSWKAVYRDRWQVSYNWKNSYKL-SVLKGHBDHVITTCLQFCGNR 275</li> <li>249 MAAAEASKAVTQPKTRSWKAVYRDRWQVSYNWKNSYKL-SVLKGHBNHVITTCLQFCGNR 275</li> <li>250 276 IVSGSDDNTLKVWSAVTGCKLRTLVGHTGGTMSLISGSLDHTIKVWNWHTGEC 335</li> <li>371 LATGSYDTTIKIMIETEECIRTLVGHTGGTMSLISGSLLHVLMGHVAAVCVQP-G 335</li> <li>367 LATGSYDTTIKIMIETEECIRTLVGHTGGTMSLESCDSKLISGSLDHTIKVWNWHTGEC 366</li> <li>367 LSTFAAHTDSVISVHFDCHLLASGSSDKTVKFFDFNSKE-TYCLKGHSDWVSTHVDIKS 425</li> <li>367 LSTFAAHTDSVISVHFDCHLLASGSSDKTVKFFDFNSKE-TYCLKGHSDWVSTHVDIKS 425</li> </ul>

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	<pre>A;Accession: \$48052 A;Molecule type: mRNA A;Residues: 1-410 <hat> A;Cross-references: EMBL:D30615 A;Cross-references: EMBL:D30615 A;Note: the tille has been revised in \$48075 A;Note: the tille has been revised in \$48075 A;Httori, M:, Adachi, H.; Tsujimoto, M.; Arai, H.; Inoue, K. Nature 370, 391-391, 1994 A;Title: Miller-Dicker lissencephaly gene encodes a subunit of brain platelet-activat A;Contents: annotation A;Contents: annotation</hat></pre>	<pre>A.NOESE this is a revision to the title from reference S48052 A.NOESE this is a revision to the title from reference S48052 B.Hattori, M. Submitted to the EMBL Data Library, April 1994 A.REFERENCE number: S31606 A.ACCESSION: S51606 A.ACCESSION: S516665 A.ACCESSION: S51666 A.ACCESSION: S51666 A.ACCESSION: S51666 A.ACCESSION: S51666 A.ACCESSION: S51666 A.ACCESSION: S51666 A.ACCESSION A.ACCESSION</pre>	Query Match14.0%Score 439; DB 2; Length 410;Best Local Similarity30.1%; Pred. No. 6.9e-27;MatchesMatches 110; Conservative 62; Mismatches 133; Indels 60; Gaps 10;Qy227 GFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHD 262111111111263 DHVITCL-OFCGNRIVSGSDDNTLKVWSAVTGKCLRFLVGHTGGWMSSOMRDNIIISG 3190v263 DHVITCL-OFCGNRIVSGSDDNTLKVWSAVTGKCLRFLVGHTGGWMSSOMRDNIIISG 319	<ul> <li>1 : : !   : !   :                        </li></ul>	<b>7</b> 2 3 7 5	<pre>RESULT 14 S36113 14 S36113 LIS-1 protein - human LIS-1 protein - human C;Species: Hono sapiens (man) C;Species: Hono sapiens (man) C;Accession: S36113 #sequence_revision 10-Nov-1995 #text_change 26-May-2000 C;Accession: S36113 #sequence_revision 10-Nov-1995 #text_change 26-May-2000 C;Accession: S36113 #sequence_revision 10-Nov-1995 #text_change 26-May-2000 A;Reiner, O.; Carrozzo, R.; Shen, Y.; Wehnert, M.; Faustinella, F.; Dobyns, W.B.; Cas Nature 364, 717-721, 1993 A;Title: Isolation of a Miller-Dieker lissencephaly gene containing G protein beta-su A;Reference number: S36113; MUID:93361119 A;Stetus: preliminary</pre>
-	QY474NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDCTVKLWDL533:1111:1:111:1:1:1111:1:1:1:1:1:1:1:1111:1:111:1:1:1111:1:11:1:1:1:1:1111:1:11:1:1:1:1:1111:1:11:1:1:1:1:1111:1:11:1:1:1:1:1111:1:11:1:1:1:1:1111:1:1:1:1:1:1:12:1:1:1:1:1:1:13:1:1:1:1:11:1:1:1:1:11:1:1:1:1:11:1:1:1:1:11:1:1:1:1:12:1:1:1:1:13:1:1:1:1:13:1:1:1:1:13:1:1:1:1:13:1:1 <td:1:1< td="">:13:1:1<td:1:1< td="">:13:1:1<td:1:1< td="">:14:1:1<td:1:1< td="">:15:1:1<td:1:1< td="">:15:1:1<td:1:1< td="">:15:1:1<td:1:1< td="">:15:1:1<td:1:1< td="">:15<td::1:1< td=""><td:1:1< td="">:15:1:1<td:1:1< td="">:15:1:1<td:1:1< td=""><td><pre>RESULT 12 A55532 myosin-heavy-chain kinase (EC 2.7.1.129) A - slime mold (Dictyostellum discoideum) C;Species: Dictyostellum discoideum C;Species: Dictyostellum discoideum C;Species: Dictyostellum discoideum C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000 A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin A;Fitle: Structural A;Fitle: Structural A; A;Fitle: Struc</pre></td><td>A;Introns: #status absent C;Superfamily: unassigned WD repeat proteins; WD repeat homology C;Superfamily: unassigned WD repeat protein; phosphoprotein; phosphotransfera C;Seyerds: autophosphorylation; coiled coil; multimer; phosphoprotein; phosphotransfera F;865-898/Domain: WD repeat homology <wd2> F;901-1022/Domain: WD repeat homology <wd3> F;1011-1022/Domain: WD repeat homology <wd5> F;1011-1022/Domain: WD repeat homology <wd5> F;1011-11022/Domain: WD repeat homology <wd5> F;1011-11022/Domain: WD repeat homology <wd5> F;1011-1112-1143/Domain: WD repeat homology <wd5></wd5></wd5></wd5></wd5></wd5></wd3></wd2></td><td>Query Match14.2%Score 446.5; DB 2; Length 1146;Best Local Similarity 33.8%, Pred. No. 7.6e-27;Best Local Similarity 33.8%, Pred. No. 7.6e-27;Second Similarity 33.8%Matches 97; Conservative 59; Mismatches 124; Indels 7; Gaps 5;QY 251 ELKSPKVLKGHDHVITCLOFCGNRIV-SGSDDNTLKVWSAVTG-KCLRTLVGHTGGWS 30811:::1:::11:::1:::112:::1:::1113::1:::1114::1:::1115::1:::1116::1:::1117Db858 DLKCVSTIQSFRERVNSIAFFDNQKLLCAGYGDGTYFRVFDVNDWKCLYTVNGHRKSIES 917003309 SQMRDNIIISGSTDRTLKVWNAETGECHHTVGHTSTVRCMHLHEKRVVSGSRDATLR 3661:17:1:1:11118IACNSNYIFTSSDDNTIKVHIIRSGNTKCIETLVGHTGEVNCVVANEKYLFSCSYDKTIK 977</td><td>Qy367 VWDIETGQCLHVLMG-HVAAVRCVQYDGRRVSGAYDFMVKVWDFETETCLHTLQGHTNR 425Db978 VHDLSTFKEIKSFEGVHTKYIKTLALSGRYLFSGRNDOIIYVWDTETLSMLFNMQGHEDW 1037Oy426 VYSLOFDGIHVVSGSLDFSIRVWDVETGNCIHTLFGHQSLTSGMELKDNILVSGNADSTV 485Oy426 VYSLOFDGIHVVSGSLDFSIRVWDVETGNCIHTLFGHQSLTSGMELKDNILVSGNADSTV 485Db1038 VLSLHCTASYLFSTSRDNVIKIMDLSNFSCIDTLKGHMNSVSSCVVKDRYLYSGSEDNSI 1097Qy486 KIWDIKFGQCLQFLQGENKHQSAVTCLQFNKNFVTSSDDGTVKLMD 532Qy486 KIWDIKFGQCLQFLQGENKHQSAVTCLQFNKNFVTSSDDGTVKLMD 532Db1098 KVWDLDTLECVYTIPKSHSLGVKCLMVFNNOIISAAFDGSIKVWE 1142</td><td>RESULT 13 S48052 platelet-activating factor acetylhydrolase 45K chain - bovine C;Species: Bos primigenius taurus (aattle) C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 26-May-2000 C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 26-May-2000 K;Hattori, M.; Adachi, H.; Tsujimoto, M.; Arai, H.; Inoue, K. Nature 370, 216-218, 1994 A;Title: Miller-Dieker lissencephaly gene encodes a subunit of brain platelet-activating A;Reference number: S48052; SU10:94405</td></td:1:1<></td:1:1<></td:1:1<></td::1:1<></td:1:1<></td::1:1<></td:1:1<></td::1:1<></td:1:1<></td::1:1<></td:1:1<></td::1:1<></td:1:1<></td::1:1<></td:1:1<></td::1:1<></td:1:1<></td::1:1<></td:1:1<></td:1:1<></td:1:1<></td:1:1<></td:1:1<></td:1:1<></td:1:1<></td:1:1<>	<pre>RESULT 12 A55532 myosin-heavy-chain kinase (EC 2.7.1.129) A - slime mold (Dictyostellum discoideum) C;Species: Dictyostellum discoideum C;Species: Dictyostellum discoideum C;Species: Dictyostellum discoideum C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000 C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-May-2000 A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin heavy chain kinase A from Dictyostellum, Evidence A;Fitle: Structural analysis of myosin A;Fitle: Structural A;Fitle: Structural A; A;Fitle: Struc</pre>	A;Introns: #status absent C;Superfamily: unassigned WD repeat proteins; WD repeat homology C;Superfamily: unassigned WD repeat protein; phosphoprotein; phosphotransfera C;Seyerds: autophosphorylation; coiled coil; multimer; phosphoprotein; phosphotransfera F;865-898/Domain: WD repeat homology <wd2> F;901-1022/Domain: WD repeat homology <wd3> F;1011-1022/Domain: WD repeat homology <wd5> F;1011-1022/Domain: WD repeat homology <wd5> F;1011-11022/Domain: WD repeat homology <wd5> F;1011-11022/Domain: WD repeat homology <wd5> F;1011-1112-1143/Domain: WD repeat homology <wd5></wd5></wd5></wd5></wd5></wd5></wd3></wd2>	Query Match14.2%Score 446.5; DB 2; Length 1146;Best Local Similarity 33.8%, Pred. No. 7.6e-27;Best Local Similarity 33.8%, Pred. No. 7.6e-27;Second Similarity 33.8%Matches 97; Conservative 59; Mismatches 124; Indels 7; Gaps 5;QY 251 ELKSPKVLKGHDHVITCLOFCGNRIV-SGSDDNTLKVWSAVTG-KCLRTLVGHTGGWS 30811:::1:::11:::1:::112:::1:::1113::1:::1114::1:::1115::1:::1116::1:::1117Db858 DLKCVSTIQSFRERVNSIAFFDNQKLLCAGYGDGTYFRVFDVNDWKCLYTVNGHRKSIES 917003309 SQMRDNIIISGSTDRTLKVWNAETGECHHTVGHTSTVRCMHLHEKRVVSGSRDATLR 3661:17:1:1:11118IACNSNYIFTSSDDNTIKVHIIRSGNTKCIETLVGHTGEVNCVVANEKYLFSCSYDKTIK 977	Qy367 VWDIETGQCLHVLMG-HVAAVRCVQYDGRRVSGAYDFMVKVWDFETETCLHTLQGHTNR 425Db978 VHDLSTFKEIKSFEGVHTKYIKTLALSGRYLFSGRNDOIIYVWDTETLSMLFNMQGHEDW 1037Oy426 VYSLOFDGIHVVSGSLDFSIRVWDVETGNCIHTLFGHQSLTSGMELKDNILVSGNADSTV 485Oy426 VYSLOFDGIHVVSGSLDFSIRVWDVETGNCIHTLFGHQSLTSGMELKDNILVSGNADSTV 485Db1038 VLSLHCTASYLFSTSRDNVIKIMDLSNFSCIDTLKGHMNSVSSCVVKDRYLYSGSEDNSI 1097Qy486 KIWDIKFGQCLQFLQGENKHQSAVTCLQFNKNFVTSSDDGTVKLMD 532Qy486 KIWDIKFGQCLQFLQGENKHQSAVTCLQFNKNFVTSSDDGTVKLMD 532Db1098 KVWDLDTLECVYTIPKSHSLGVKCLMVFNNOIISAAFDGSIKVWE 1142	RESULT 13 S48052 platelet-activating factor acetylhydrolase 45K chain - bovine C;Species: Bos primigenius taurus (aattle) C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 26-May-2000 C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 26-May-2000 K;Hattori, M.; Adachi, H.; Tsujimoto, M.; Arai, H.; Inoue, K. Nature 370, 216-218, 1994 A;Title: Miller-Dieker lissencephaly gene encodes a subunit of brain platelet-activating A;Reference number: S48052; SU10:94405

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RESULT 15 746032 W-40 repeat regulatory protein tup1 homolog - Arabidopsis thaliana Ny Alternate names: protein T16K5.10 C:Species: Arabidopsis thaliana (mouse-ear cress) C:Species: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 26-May-2000 C:Accession: T4603 C:Accession: T4603 R:Rieger, W.; Gabel, C.; Mueller-Auer, S.; Schaefer, M.; Z1pp, M.; Mewes, H.W.; Lemcke, submitted to the Protein Sequence Database, January 2000 A:Reference number: 223015 A:Accession: T4603 A:Accession: T4605 A:Accession: T16K5 A:Accession: T16K5 A:Accession: 3 A:Accession: 4 Accession: 4 Accession Acces 7; 12; 485 ECIHTLYGHTSTVRCMHL - - HEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQ - 390 

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 432 ----DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD--NILVSGNADSTV Query Match 13.1%; Score 410.5; DB 2; Length 317; Best Local Similarity 31.9%; Pred: NO. 8.4e-25; Matches 98; Conservative 66; Mismatches 106; Indels 37; 35; Length 409; 486 KIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKN--FVITSSDDGTVKLWDLK 534 proteins; WD repeat homology 13.9%; Score 436.5; DB 2; Length 4 34.0%; Pred. No. 1.1e-26; :1ve 54; Mismatches 103; Indels I: WD repeat homology <WD1>
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- Db 195 DDENPPVSFVRFSPNGKFILVGTLDNTLRLWNISSAKFLKTYTGHVNAQYCISSAFSVTN 254
- QY 468 GMELKDNILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGT 527
  - Db 255 GKR-----IVSGSEDNCVHMWELNSKKLLDQKLEGHTETVMNVAC-HPTENLIASGSLDKT 308
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332 10.6 704 1 T2D4_DROME 330 10.5 486 1 PRL_ARATH 330 10.5 577 1 TBLL_HUMAN 326 10.4 2295 1 WDR9 HUMAN	323.5 10.3 332 1 GBLP_DICDI 746800 dict. 318.5 10.1 713 1 TUP1_YEAST P16649 sacc	012417 015542 015736 039190	312 9.9 659 1 YK16_YEAST 311.5 9.9 682 1 TUP1_KLULA	ALIGNMENTS	SULT 1 10_CAEEL	SE10_CAEEL STANDAR Q93794;		N. B12.3. s elegans tazoa; Né					CC -!- SIMILARITY: CONTAINS 1 F-BOX DOMAIN. CC -!- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).		the European Bioinformatics Institute. There are no restriction		entities requires a license agreement (See http://www.isb-sib.c		DR EMBL; Z79757; CAB02129.1; DR WormPeo: F55B12.3: CE16120.	DR InterPro; IPR001680; -		DR Pfam; PF00400; WD40; 7. DR PRINTS; PR00320; GPROTEINBRPT.	DR PROSITE; PSS0181; FBOX; 1.	PROSITE; PS50082; WD_REPEATS_2; 7.	DR PROSITE; PS50294; WD_REPEATS_REGION; 1. KW Repeat: WD repeat.	FT DOMAIN 113 159 F-BOX,	REPEAT 286 316	FT REPEAT 328 356 WD 3. FT REPEAT 368 396 WD 4.	REPEAT 408 438 DEDEAT 453 481	REFEAT 4.03 4.01 WU REPEAT 4.93 5.22 WD REPORTENCE 5.70 3.0 6.0.75 Mai. 0	SEQUENCE 3/9 AA; 042/3 MW;
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compug	in search, using sw model	September 25, 2001, 14:41:35 ; St (wii 188	S-09-328-877A-8 143 MSKPGKPTLNHGLVPVDLKS	BLOSUM62 Gapop 10.0 , Gapext 0.5	34255486 r	ts satisfying chosen parameters	length: 0 length: 200000000	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	SwissProt_39:*	che number of results predi than or equal to the score by analysis of the total	SUMMARIES	Length DB ID	579 1 684 1 605 1	7 640	2242	a 701	3 605 1 5 518 1	7 775 1	779 1 5 1356 1	3 650 1 4 732 1	362	2 1146 1	0 409 1 0 409 1	1 600	6 267 1 5 376 1	5 422 1	422	501 1 515 1	5 395 1693	3 444 1 2 714 1	473 473
J	OM protein - protein	Run on: Se	Title: US Perfect score: 31 Sequence: 1	Scoring table: BI Ga	Searched: 93	Total number of hits	Minimum DB seq leng Maximum DB seq leng	Post-processing: Mi Ma Li	Database : Sw	Pred. No. is the r score greater than and is derived by		score	1 1238 39 2 725.5 23 3 680 21	650	641.5	639.5	638 634 5	620	618.5 582.5	576.5 516	461	400 446.5	439	438	403396	392.5 383	376.5	376 365	361 360	353 353	342.5

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<pre>Duery Match 39.4%; Score 1238; DB 1; Length 579; Best Local Similarity 45.6%; Pred. No. 9.4e-90; Matches 262; Conservative 85; Mismatches 162; Indels 66; Ga 55 DHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDLRAANGOGOQRRRITSV 111 111 111 111</pre>	DU 23 DNGEE-SSISNGSSSINADKLSSSRPLQHKLDLSASPSRNNDLNPR 68 OY 111 OPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFPQRDFISLLPKEL 170 : : : 1   1   1 DD 69VEHLIALFKDLSSAEQMDAFTRLLQESNMTNIRQLRAIIEPHFQRDFLSCLPVEL 123	Qy       171       ALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEE       210         :       :       !       !       !         Db       124       GMKILHNLTGYDLLKVAQVSKNWKLISEIDKIWKSLGVEEFKHHPDPTDRVTGAWQGTAI       183	QY       211      GIDEPLHIKRRKVIKPGFIHSPWKSAYIRQHRIDTWWRGELKSPKVL       258         I       I       I       I       I       I         Db       184       AAGVTIPDHIQPCDLNVHRPLKLOKEGDIFERAADKSRYLRADKIEKNWNANDIMGSAVL       243	<pre>QY 259 KGHDDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGRCLRTLVGHTGGVWSSQMRDNII 316</pre>	<pre>Qy 317 ISGSTDRTLKVWNAETGECIHTLYCHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGOCL 376</pre>	QY 377 HVLMGHVAAVRCVQYDGRRVVSGAVDFMVKVWDFEFETCLHTLQGHFURVYSLQFDG1H- 435 1	<pre>Qy 436 -VVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIK 491</pre>	Qy       492       TGQCLQTLQGPNKHQSAVTCLQ-FNKNFVITSSDGTVKLMDLKTGEFIRNLVTLESGGS       550         l	QY 551 GGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDFD 585 11 :11: :::1 † 111111 11111:::1111 Db 541 GGCIWRLCSTSTMLACAVGSRNNTBETKVILLDFD 575	RESULT 2 CC4_CANAL ID CC4_CANAL STANDARD; PRT; 684 AA.		GN CDC4. OS Candida albicans (Yeast). OC Bukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; OC Sarcharomyceralae: nitoconoric Sarcharomycotila; Saccharomycetes;	NCBL_TAXID=5476; [1] SEQUENCE FROM N.A.	Shieh J.C., White A.M., Rosamond J.; Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases. -1- FUNCTON: THIS PROTEIN IS ESSENTIAL FOR INITIATION OF DNA	CC POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE BUDD LES TO FORM THE CC POLES OF THE MITOTIC SPINDLE. IT ALSO PLAYS A ROLE IN BUD CC DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND CC DEVELOPMENT, FUSION OF ZYGOTICNUCLEI AFTER CONJUGATION AND CC MARNEDATENTON FUSION OF ZYGOTICNUCLEI AFTER CONJUGATION AND	CC -1'EXMELARITY: CONTAINS (BY SIMILARITY). CC -1' SIMILARITY: CONTAINS 1 FUOX DOMAIN. CC -1' SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS). CC

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Db 118 SFRILSFLDARSLCQAAQVSKHWKELADDDVIWHRMCEQHINRKCEKCGWGLPLLERNTL	210BGIDEPLHIKRKVIKP	Db 178 YAAKASIQKRYERLTKRGVDQAHESSPVKRAKLDDYPTSSNEETISSVKPPSPNSDSKFF 237 Qy 227 -GFIHSPWKSAYIRQHRLDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSDDNTL 285         :  :::     :       :       :       :       :          :         :         :         :         :         :         :         :         :         :         :         :         :         :       :         :         :         :         :         :         :         :         :         :       :       :       :       :	Db 238 LPFKTRPWKEVYAERCRVECNWRHGRCRQ-VVLSGHSDGVM-CLQLVRNILASGSYDATI 295 0v 286 KVWSAVTGKGLRTLVGHTGGVWSSOMRDNITISGSTDFFLKVWMAAFTGFGTHHTLYGHTSG 345	200 NYMAATIGAALAALAALAALAALAALAALAALAALAALAALAALAAL	Qy       346       VRCMHLHEKRVVSGSRDATLRVMDIETGQCLHVLMGHVAAVRCVQY - DGRRVVSGAYDF 403         0       346       VICLTFDSTLLVSGSADCTVKLMHFSGGKRI-TLRGHTGPVNSVRIIRDRGLVLSGSDDS 414	QY 404 Db 415	Commentation of the second sec	07 522	rough a collaboration Db 528 GSEDGKIYLW 537 he EMBL outstation -	RESUL MT30_ ID	AC P39014; DT 01-FEB-1995 (Rel. 31,	01-FEI 01-OC MET30		charomycetales; Saccharomycetaceae; Saccharom I_TaxID=4932;	RN [1] RP SEQUENCE FROM N.A. RC STRAIN-X2180-1A:	RX MEDLINE-96069360; PubMed=8524217; RA Thomas D., Kuras L., Barbey R., Cherest H., Blaiseau P.L.,		RI MOLVETIONING, IS AN ESSENTIAL PROTEIN WITH WD40 repeats."; RL MOL.Cell.Biol. 15:6526-6534(1995). RN [2]	RP		RA Louis E., Lye G., Moule S., Moule T., Odell C., Péarson D., RA Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., RA Walsh S.V., Whitehead S.;	SV 110 RL Subm :1 CC -1-	AV 66 EL 170	
	STANDARD; PRT; 605 AA.	(Rel. 36, Created) (Rel. 36, Last sequence update) (Rel. 40, Last annotation update)	F-BOX/WD-REPEAT PROTEIN POF1. POF1 OR SPAC57A10.05.C. Schizosaccharomyces pombe (Fission yeast).	Eukaryota; Fundi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces.	NCBI_TaxID-4896; [1] SEQUENCE FROM N.A.	STMAIN=91.2; Katayama S., Kitamura K., Toda T.; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases [2]	SEQUENCE FROM N.A. STRAIN=972; Badcock K., Churcher C.M., Wood V., Barrell B.G., Raj Submitted (APR-1997) to the EMBL/GenBank/DDRJ Garabas.		This SWISS-PROT entry is copyright. It is produced through a co between the Swiss Institute of Bioinformatics and the EMBL o the European Bioinformatics Institute There are no restricti	use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/	to license@isb-sib.ch).	EMEL: 2942410, PANGALOBIL: EMEL: 294644, CABOBI66.1; Interpro: IPROO1680;	PTOS IPRUOIBUD: - PEPGO405 F-DAX; 1. PF00406; WD40; 7.	PR00320; GPROTEINBRPT. PS50181; FB0X; 1. PS50181; FB0X; 1.	PS000 8; WD_REPEATS_1; 2. PS50082; WD_REPEATS_2; 7. PS50294; WD_REPEATS_REGION; 1.	repeat. 107 153 F-BOX.	259 WD L. 339 WD 2. 330 GD 2.	420 WD 460 WD	500 WD 538 WD	/TTRC33/AEC2CTE0	<pre>/ Match 21.6%; Score 680; DB 1; Length 605 Local Similarity 29.8%; Pred. No. 7.1e-46; hes 164; Conservative 93; Mismatches 181; Indels</pre>	CSATPTTFGDLRA	KKEGUQSISVSAFNISSMHNELSGLSEKSRQRVE QPPTGLOEWLKMFOSWSGPEKLLALDELIDSCEPTOVKHMMOVIEPOFORDFISIJIDK	

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GMELKDNILVSGNADSTVKIWDIKTGQCLQT-----LQGPNKHQ-----SAVTCLQ 513

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οy between the Swiss Institute of Bioinformatics and the EMBL outstation -the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities reguires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch). 18; 496 229 429 497 MIDGADESDTPSNEQETVLDENIPYPTHLLLSCGLDNTIKLWDVKTGKCIRTQFGHVEGVW 556 67 KKPC-----KVSEYTSTTGLVPCSATPTTFGDLRAANGQGQQRRRITSVQPPTGLQEWL 120 121 KMFQSWSGPEKLLALDELID-SCEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLE 179 230 HS------PWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVS 278 279 GSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHT 338 || |:|: :| ||| :| || || :| : | :|:|| :|:|| ||||| ||||| | GSYDSTIGIWDLFTGKLIRRLSGHSDGVKTLYFDDRKLITGSLDKTIRVWNYITGECIST 377 108 HTACYKODLKRTQEINANIAKLP ..... 141 339 LYGHTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGR--RV 396 ------IHVVSGSLDTSTRVWDVETGNCIHTLTGHQSLTS 467 Gaps PTLNHGLVPVDLKSAKEPLPHQTVMKIFSISIIAQGLPFCRRRMKRKLDHGSEVRSFSLG 66 PKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEP - - - - - - - - - - - - LHIKRKVIKPGFI 437 FSCSDDTTIRMWDIRTNSCLKVFRGHVGQVQKIIPLTIKDVENLATDNTSDGSSPQDDPT Query Match 20.7%; Score 650; DB 1; Length 640; Best Local Similarity 26.4%; Pred. No. 1.8e-43; Matches 163; Conservative 114; Mismatches 197; Indels 144; -> I (IN REF. 1). 5135D4BCA2E1EB97 CRC64; PRINTS; PRO0320; GPROTEINBRPT. PROSTTE; PS00678; WD\_REPEATS\_1; 4. PROSTTE; PS00678; WD\_REPEATS\_2; 6. PROSTTE; PS00679; WD\_REPEATS\_2; 6. PROSTTE; PS50294; WD\_REPEATS\_2; 6. PROSTTE; PS50294; WD\_REPEATS\_REGION; 1. Transcription regulation; Methionine biosynthesis; Cystelie biosynthesis; Repeat. WD repeat. DOMAIN 181 227 F-BOX. WD 1... WD 2. WD 3. WD 5. WD 5. WD 8. WD 9. WD 9 397 VSGAYDFMVKVWDPETETCLHTLQGHTNRVYSL-------EMBL; 246861; CAA86905.1; -. EMBL; L26505; AAA96717.1; -. SGD; 50001308; MET30. InterPro; IPR001680; -. InterPro; IPR001810; -. Pfam; PF00460; F-box; 1. Pfam; PF00400; WD40; 6. : MW 61 72835 1 368 449 4499 538 538 635 640 AA; 430 QFDG-------181 300 340 340 419 5509 5509 5509 607 CONFLICT SEQUENCE REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT REPEAT 180 ~ 318 2 q oγ g ò qq δ q δ q Db Db δ q  $\delta$ q δ ٦đ

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QY	514 FNKNEVITSSDDGTVKLW 531
Dþ	617 IGDSECFSGDEFGCVKMY 634
assurvester and an anticester	LT 5 LEBENI STANDARD; LEBENI STANDARD; SCOB_EMENI STANDARD; 15-JUL-1998 (Rel. 36, Last 15-JUL-1998 (Rel. 36, Last 51-JUL-1998 (Rel. 36, Last SULFUR METABOLITE REPRESSIO SECOND OR MAPBI. Emericella nibulans (Asperg Eurotiales; Trichocomaceae; NCBL_TAXID=5072; CONTAINS (Asperg Eurotiales; Trichocomaceae; 11] SECURCE FROM N.A. SECURCE 678 AA; 76070 M SECURCE 678 AA; 70070
Ϋ́Ψ.	86; Mismatches 210; Indels 172; Gaps
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<ul> <li>0Y 101 GOORRHISYOPPICKEGGEUIKNEGSWGORKLIALDELIDEGE</li> <li>03 PDOKCRFOADEPSMDKLORELESLPGGDOGISHW-SLFSANPAKHRKLILGGEIMAGC</li> <li>04 PTOVKHWOVIEPOTROLIRUDITALPEZIARILYULSFLERKDLLOADOTCRYWRILAEDNLLM</li> <li>05 POUSTISANYBDLIRUDITALPEZIARILYULSFLERKDLLOADOTCRYWRILAEDNLLM</li> <li>04 14 PTOVKHWOVIEPOTROLIRUDITALPEZIARIZCASOYSGAWAADODTWA</li> <li>05REXCREGIDEDHIKRR</li></ul>
<pre>QY 101 GQORRITSVQPPGLQEWLKW DD 700000000000000000000000000000000000</pre>

is copyright. It is produced through a collaboration stitute of Bioinformatics and the EMBL outstation -matics Institute. There are no restrictions on its institutions as long as its content is in no way tement is not removed. Usage by and for commercial icense agreement (See http://www.isb-sib.ch/announce/ icense@isb-sib.ch) ------WD 1. WD 2. WD 2. WD 4. WD 5. WD 6. WD 7. WD 8. WD 9. TOUTOURIE AND DESCRIPTION OF FOULTING AND TOUTTURATION AND DESCRIPTION. A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX. TON: CYTOPLASHIC (POTENTIAL). CTUS: 3 ISOPORAS; A, B AND C (SHOWN HERE); ARE NATIVE SPLICING. **BLIDSCEPTQVKHMMQVIEPQFQRDFISLLPKE----LALYVL 175** IQDIETIESNWRCGRHNLQRIQCRSENSKGVYCLQYDDEKIIS 255 W-RILAEDNL--------LWREKCKEEGIDEPLHIKRR 221 YIRQHRIDTNWRRGELKSPKV-LKGHDDHVITCLQFCGNRIVS 278 LRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHT 338 Gaps ding sequences of unidentified human genes. X. s of 100 new CDNA clones from brain which can is in vitro."; 98). Y RECOGNIZE AND BINDS TO SOME PROTEINS AND REPEATS\_1; 5. REPEATS\_2; 7. REPEATS\_RECION; 1. REPEATS\_RECION; 1. REPEAT; WD repeat; Alternative splicing. 7 0.4%; Score 641.5; DB 1; Length 542; 2.1%; Pred. No. 6.5e-43; ve 89; Mismatches 177; Indels 37; INS 1 F-BOX DOMAIN. INS 7 WD REPEATS (TRP-ASP DOMAINS). 1528.1; -. 2329.1; -. 2330.1; -. 2331.1; -. 2331.1; ALT\_INIT. Ohara O.; CEINBRPT. (WM 060 ::

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Db316LIHHNEAVLHLRFSNGLMVTCSKDRSIAVWDMASATDITLRRVLVGHRAAVNVVDFDDKY375QY396VVSGAYDFWVKWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSSLDTSIRVWDVETGNC455Db376IVSGAYDFMVKWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSSLDTSIRVWDVETGNC455Db376IVSGAYDFMVKWSTSTCEFVRTLNGHKRGIACLQYRDRLVVSGSSDNTTRLWDIECGAC435QY456IHTLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGOCLQTLQGPNKHQ506QY456IHTLTGHQSLTSGMELKDNILVSGANDGKIKVWDLQAALDPRAPASTLCLRTLVEHS492QY507SAVTCLQFNKNEVTSSDDGTVKLWD532QY507SAVTCLQFNKNEVTSSDDGTVKLWD532QY507SAVTCLQFNKNEVTSSDDGTVKLWD532QY903GRVFRLQFDEFQIISSSHDDTLLIWD518RESULT77703DD1936Rel1.36.703CO141700STANDARD;PRT;703AA.0411700STANDARD;PRT;770415-70U-1998Rel1.36.715-70U-1998Rel1.36.Created)	<pre>DT 15-UUL1998 (Rel: 30, Leaded) DT 15-UUL1998 (Rel: 30, Last sequence update) DT 01-OCT-2000 (Rel: 40, Last annotation update) DN 022 OR SUD1 OR SPAC4D7.03. Schizosaccharomyces pombe (Flssion yeast). OS Schizosaccharomycetales; Schizosaccharomycetes; Schizosaccharomyces. OC Schizosaccharomyces. Schizosaccharomyces. Schizosaccharomyces. Schizosaccharomyces. Schizosaccharomyces. NUBL_TaxID-44966; NI 11 RP SEQUENCE FROM N.A. RP 23 Numitted (DEC-1997) to the EMBL/GenBank/DDBJ databases. RN 2411 P.V., Tten D., Kelly T.J.; RA 24114 D.V. Tten D., Kelly T.J.; Sud1+ targets cyclin-depadent kinase-phosphorylated Cdcl8 and Rum1 Proteins for degradation and stops unwanted diploidization in fission Numer Proteins for degradation and stops unwanted diploidization in fission</pre>	<pre>RL Proc. Natl. Acad. Sci. U.S.A. 95:8159-8164(1998). R1 31 RP SEQUENCE FROM N.A. F20UENCE STAIN-972; F20UENCE C.M.: Barrell B.G., Rajandream M.A., Wood V.; F20UENCE STAIN-972; F20UENCE C.M.: Barrell B.G., Rajandream M.A., Wood V.; F20UENCE STAIN-977; F20UENCE C.M.: Barrell B.G., Rajandream M.A., Wood V.; F20UENCE STAIN-972; F20UENCE C.M.: Barrell B.G., Rajandream M.A., Wood V.; F20UENCE STAIN-972; F20UENCE C.M.: Barrell B.G., Rajandream M.A., Wood V.; F20UENCE STAIN-972; F20UENCE C.M.: Barrell B.G., Rajandream M.A., Wood V.; F20UENCE STAIN-972; F20UENCE C.M.: Barrell B.G., Rajandream M.A., Wood V.; F20UENCE STAIN-972; F20UENCE C.M.: Barrell B.G., Rajandream M.A., Wood V.; F20UENCE STAIN-972; F20UENCE STAINES F20UENCE F20UENCE TAINES F20UENCE FROM FAILS F20UENCE F18: F1000 F2018 F20UENCE F20UENCE F3000AINS). F20UENCE F3000AINS F20UENCE F3000AINS F20UENCE F3000AINS F20UENCE F3000AINS F20UENCE F3000AINS). F20UENCE F3000AINS F20UENCE F3000AINS F20UENCE F3000AINS). F20UENCE F3000AINS F20UENCE F3000AINS F20UENCE F300AINS F20UENCE F3000AINS F20UENCE F300AINS F20UENCE F30UENCE F300AINS F20UENCE F300AINS F20UENCE F30UENCE F300AINS F20UENCE F300AINS F20UENCE F30UENCE F30UENCE</pre>	CC EMBL: AF03867; AAB95480.1; - DR EMBL: AF03867; AAB95480.1; - DR EMBL: 298602; CAB11275.1; - DR InterPro: IPR001680; - DR InterPro: IPR001680; - DR Pfam: PF00646; F-box; 1. DR Pfam: PF006046; F-box; 1. DR Pfam: PF00600; WAD0; 6. DR PRINTS: PS0010; WDC FROTEINBPT. DR PRNTTE: PS00120; GFROTEINBPT. DR PROSITE: PS50082; WD_REPEATS_21; 6. DR PROSITE: PS50082; WD_REPEATS_21; 6. DR PROSITE: PS50082; WD_REPEATS_21; 6. DR PROSITE: PS50082; WD_REPEATS_21; 6.
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JLT 9 A_HUMAN FWIA_HUMAN STANDARD; PRT; 605 AA. 09Y297; 09Y213;	01-CCT-2000 (Rel. 40, Created) 01-CCT-2000 (Rel. 40, Last sequence update) 01-CCT-2000 (Rel. 40, Last anotation update) F-BOX/WD-REPEAT PROTEIN 1B (F-BOX AND WD-REPEATS PROTEIN BETA-TRCP)	E (E3ISIKAPPAB) (PIKAPPABALPHA-E3 RECEPTOR SUBUNIT). N FEXULA OR FBUIA OR BTRCP OR BTRC. S Homo sapiens (Human). C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	NCBL_IAXID-9000; [1] SEQUENCE FROM N.A. (ISOFORM 1). VERTING-00071530, D.L.M.J.OCEONO.	meDurus=990/33395; ruomed=9839996; Yaron A., Hatzubai A., Davis M., Lavon I., Amit S., Manning A.M., Andersen J.S., Mann M., Mercurio F., Ben-Neriah Y.; "Identification of the receptor component of the IkappaBalpha-	ubiquitin ligase."; Nature 396:590-594(1998). [21]	SEQUENCE FROM N.A. (ISOFORM 2). TISSUE-Lymphoid;	MEDLINE-99325370; PubMed-9560940; Margottin F., Bour S.P., Durand H., Selig L., Benichou S., Richard V., Thomas D., Strebel K., Benarous R.; "A novel human WD protein, h-beta TrCp, that interacts with HIV-1 Vpu	шост	SEQUENCE FROM N.A. (ISOFORM 2). Cenciarelli C., Chiaur D.S., Guardavaccaro D., Parks W., Vidal M., Pagano M :	"Identification of a family of human F-box proteins."; Curr. Biol. 9:1177-1179(1999). [4]	CHARACTERIZATION. WINSTON J.T., Strack P., Beer-Romero P., Chu C.Y., Elledge S.J.,	<pre>"artper o' w.; "The SCF(beta-TRCP)-ubiguitin ligase complex associates specifically with phosphorylated destruction motifs in I-kappa-B-alpha and</pre>	beta-catenin and stimulates I-kappa-B-alpha ubiquitination in vitro."; Genes Dev. 13:270-283(1999). ETIMONION: DIANG SDEATETATIV MO DUSCHONDATIANDED IN ALDUA	TE FUNCTIONE FILTER DEOPENDATION TO FUNCTION INTERNAL (FIKAPPABALPHA) AND PHOSPHORYLATED BETA-CATENIN AND PROMOTES THEIR UBIOUTTINATION AND DEGRADATION.	-!- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX. -!- SUBCELLULAR LOCATION: CYTOPLASMIC.	-1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; 1 (SHOWN HERE) AND 2; ARE PRODUCED BY ALTERNATIVE SPLICING. -1- CINITADIANC CONMATING 1 PLONDAND	 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -	the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way making and this content is in no way	modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).	EMBL; AF101784; AAD08702.1;	EMBL: 114123; CAN/42/211; Embl: AF129530; AAF04464.1; MIM: 603402;	InterPro; IPR001680; InterPro; IPR001810; Pfam; PP00646; Prbox; 1. Pfam: PP00400; wuAdo.?
RESULT 9 FWIA_HUMAN ID FWIA_ AC 09129		E E E E E E E E E E E E E E E E E E E	RN [1] RP SEQUE	RA MEDUL RA YATON RA ANGEN			RX MEDLI RA Thoma RT "A no RT "A no			RT RL RN									CC MODII CC entit			DR Inter DR Inter DR Pfam; DR Pfam;
		the European Bioinformatics or Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to licenseabio-sth on	 			•					134; COUSEIVACIVE BU; MISMATCNES 16/; INDELS 59; Gaps . WSGPERIIAIDRCEPERDVEHMMOVIEDDEODDETELEDEERATIVE CEEDEMENTED 106		REKCKE 209			FNYDVNIKKDKLDQLILMHVFYSKLYPKIIKDIHNIDNNKKGNYKMTKINCQSENSK 259 VITCLOFCGNBIVSGSDDWFIKVWGAVTGKVIETVGHTGSVWSSAMDDMIIISGSENDF 323	 	<pre>::II: IIIII II I I : :II: I: III: :: III: :: II: VRVWDVETGECIKTLIHHCEAVLHLRFANGIMVTCSKDRSIAVWDMVSPRDITIRRVLVG 379</pre>		HRAAVNVUPEDDRYIVSASGDRTIKVWSMDTLEEVRTLAGHRRGIACLQYRGRLVVSGSS 439 DrsirvwDvergnvihtirchosirggmetkinnivsgnadgevktmintwron 404	DPRALSS	

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<pre>RN [1] R 5EQUENCE FROM N.A. SEQUENCE FROM N.A. RX MEDLINE=93330289; Pubmed=8393141; RA Spevak W., Keiper B.D., Stratowa C., Castanon M.J.; RA Spevak W., Keiper B.D., Stratowa C., Castanon M.J.; ranaphase are rescued by Xenopus cDNAs encoding N-ras or a protein RT anaphase are rescued by Xenopus cDNAs encoding N-ras or a protein RT with beta-transducin repeats.' Noi. Cell. Biol. 13:4953-4966(1993). RI MOI. Cell. Biol. 13:4953-4966(1993). RP SEQUENCE OF 302-518 FROM N.A. RY MEDLINE=97109804; Pubmed=8952061; RA Hudson J.W., Alarcon V.B., Elinson R.P.; RA Hudson J.W., Alarcon V.B., Elinson R.P.; R1 dentification of new localized RNAS in the Xenopus oocyte by R1 differential display PCR."; R1 Dev. Genet. 19:190-198(1996). CC -1 FUNCTION: PROMENZE AND BINDS TO SOME PHOSPHARVLATED CC -1 FUNCTION: PROMENZE AND BINDS TO SOME PHOSPHARVLATED CC -1 PROTEINS AND PROMENZE AND BINDS TO SOME PHOSPHARVLATED</pre>	<pre>CC -!- SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX CC '! SUBUNIT: PART OF A SCF (SKP1-CULLIN-F-BOX) PROTEIN LIGASE COMPLEX CC '! DEVELOPMENTAL STAGE: PRESENT IN FULLY GROWN AND PROGESTERONE- MATURED OOCYTES. THE LEVEL CHANGE VERY LITTLE EVEN AFTER ZYGOTIC CC GENE TRANSCRIPTION BEGINS FOLLOWING THE MIDBLASTULA TRANSITION. DO NOT INCREASE IN ABUNDANCE IN THE GASTRULA, NEURULA, TALLBUD, OR CC TADPOLE EMBRYO. ON AND NEUGENLA, NEURULA, TALLBUD, OR CC TADPOLE EMBRYO. TO NOMAIN. CC '- 'SIMILARITY: CONTAINS 1 F-BOX DOMAIN. CC '- SIMILARITY: CONTAINS 1 F-BOX DOMAIN. CC '- SIMILARITY: CONTAINS 1 F-BOX DOMAIN. CC '- SIMILARITY: CONTAINS 1 F-BOX DOMAIN. CC ' SIMILARITY: STRONG, TO C.ELEGANS K10B2.1. CC ' SIMILARITY: STRONG, TO C.</pre>	DR EMBL; M92268; AAA02810.11 DR EMBL; M63921; AAB49671.11 DR InterPro; IPR001800; DR Pfam; PF00646; F-box; 1. DR Pfam; PF00400; WD40; 7. DR PROSTTE; PR001320; GPROFINBRFT. DR PROSTTE; PR001320; GPROFINBRFT. DR PROSTTE; PS500132, WD_REPEATS_1; 6. DR PROSTTE; PS50012; WD_REPEATS_1; 6. DR PROSTTE; PS50012; WD_REPEATS_2; 7. DR PROSTTE; PS50012; WD_R	CONFLICT 302 304 GEN CONFLICT 302 304 GEN CONFLICT 516 518 AA; 59507 MW; 2 Best Local Similarity 31.1%; Pre Matches 161; Conservative 90; 60 VRSFSLGKKPCKVSEYTSTTGLVPCSP 1 MEGFSCSLQPPTASEREDCNNDEPPRH 114 TGLQEWLKMFOSWSGPEKLLALDELIC 61 KEKELCVKFEQWSECDQVEFVEHLIS
DR PRINTS: PR00320; GPROTEINBRPT. DR PROSITE; PS00320; GPROTEINBRPT. DR PROSITE; PS00081; WD_REPEATS_1; 6. DR PROSITE; PS00678; WD_REPEATS_2; 7. DR PROSITE; PS0082; WD_REPEATS_REGION; 1. KW Ubiquitin conjugation; Repeat; WD repeat; Alternative splicing. FT REPEAT 301 338 WD 1. FT REPEAT 311 378 WD 1. FT REPEAT 331 418 WD 2. FT REPEAT 461 WD 2. FT REPEAT 461 WD 5. FT REPEAT 553 590 WD 7. FT REPEAT 550 590 FT REPEAT 550 590 FT REPEAT 550 700 7. FT REPEAT 550 700 700 700 700 700 700 700 700 700	Query Match20.3%; Score 638; DB 1; Length 605;Best Local Similarity30.8%; Pred. No. 1.4e-42;Matches 166; Conservative 92; Mismatches 209; Indels 72; Gaps 15;Qy56 HGSEVRSFSLGKKPCKVSEYTSTGLVPCSATPTFGDLRAA 97:   :  ::   : : ::   : : ::   : : ::   : : ::  :: : ::  :: : ::  :: : : ::  :: : : :: : :: : : : : : : : : : :: : : : : : : : : : : : : : : : : : :	<pre>Db 231 RWYFDSLWRGLAERRGWGOYLFKNKPPDGNAPPNSFYRALYFKILQDIETIESN 285 0Y 247 WRRGELKSFKV-LKGHDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGG 305 11 1 11111111111111111111111111111111</pre>	SULT 10 SULT 10 TRCB_XENLA STANDARD; PRT; 518 AA. 091854; P70037; P70038; 15-UUL-1998 (Rel. 36, Created) 15-UUL-1998 (Rel. 36, Created) 15-UUL-1998 (Rel. 36, Last sequence update) 01-CCT-2000 (Rel. 40, Last annotetion update) 01-CCT-2000 (Rel. 40, Last annotetion update) 8ETA-TRCP (BETA-TRANSDUCIN REPEAT-CONTAINING PROTEIN). FBXWH OR BTRCP. Xenopus laevis (African clawed frog). Xenopus laevis (NCHL_TaxID=8355; NCHL_TaxID=8355;

CC or send an email to license@isb-sib.ch).	DR EMBL; Y08391; CAA69671.1; DR EMBL; AL022103; CAA17898.1; DR InterPro; IPR001680; DR InterPro; IPR001810; DR Pfam; PF00466; F-box; 1. DR Pfam; PF00400; WD40; 6.	PRINTS; PR PROSITE; P PROSITE; P PROSITE; P PROSITE; P		KEFEAT 05/ 08/ WU 5. SEQUENCE 775 AA; 87816 MW; B06EDBA46553EEC1 CRC64; Query Match 19.7%; Score 620; DB 1; Length 775 Best Local Similarity 27.5%; Pred. No. 5.2e-41;	100; Mismato ASGPEKL 1 11 ESFEKLPESVRC	159 QRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYW-RILAEDNLLW 20 1:1:1:1 1:1:1 1:1:2 297 QKNFLTGFPAETTNLVLTHLDAPSLCAVSQVSHHWKLVSSNEELWKSLFLKDGFFWDSI 35	QY 204REKCKEEGIDEPLHIKRRKVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLK 259       :     : : :   Db 357 DSKIRTMCLEQSLSACAIMKRVYFRHFNLRERWLHAPEKIK 397	QY 260 GHDDHVITCLOFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDN 314 260 GHDDHVITCLOFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDN 314 298 RCSFPIHGVRLITKLQFDDDKIIVSTCSPRINIYDTKTGVLIRSLEEHEGDVWTFBYVGD 457	QY 315 IIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKR 355 :::      ::  :   :   :   :   :   :   :	QY 356VVSGSRDATLRVWDIETGQCL	QY 381 GHVAAVRCQYDGRRVVSGAYDFWVKVMDFETETCLHTLQGHTNRVYSLQFDGIHVVS 438 	QY       4.39       GSLDTSIRVWDVETGNCIHTLFGHQSLFSGMELKDNILVSGNADSTVKIWDIKTGQCL       4.96         D       1	QY 497 QTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGSGGVWR 556 1:1 1 1:1:1:1:1:1:1:1:1:1:1 Db 695 DILKCPLGHIFFQHDESKVVSGS-HSTLQLWDIRSGKLVRDLLTDLDIIWQ 744	QY 557 IRASNTKLVCAVGSRN 572 2 1 1 1 2 745 VAYNENVCVAAVLRNN 760	RESULT 12 CC4_YEAST ID CC4_YEAST STANDARD; PRT; 779 AA. AC P07834; DT 01-AUG-1988 (Rel. 08, Created)
<ul> <li>170 LALYVLSFLEPKDLLOAAOTCRYWRIIAEDNLLWREKCKEEGIDEPLHTKRR 221</li> </ul>	11       11 <td< td=""><td><ul> <li>267 TCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK</li> <li>111: 111111111111111111111111111111111</li></ul></td><td>35 38</td><td>444</td><td><pre>Qy 495 CLQTLQGPNKHQSAYTCLQPNKNFYITSSDGTVKLWD 532   :   :      :: :::   {  :: ] Db 476 CLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWD 510</pre></td><td></td><td>DT 15-JUL-1998 (Rel. 36, Created) DT 15-JUL-1998 (Rel. 36, Last sequence update) DT 01-OCT-2000 (Rel. 40, Last annotation update) DE WD-REPEAT PROTEIN POP1.</td><td>Schizose Schizose Schizose</td><td></td><td>MEDLINE-972; PubMed=9203581; Kominami K., Toda T.; Fisision yeast WD-repeat protein popl regulates genome ploidy t</td><td>did the S-phase initiator Cdc18."; (Genes Dev. 11:1548-1560(1997). [2]</td><td></td><td>CC TIC FUNCTION INVESTIGATION OF CAR INTERFACE OF FUNCTION FUNCTEADOME CC DEPENDENT DEGRADATION OF CAR INTERFOR RUM AND S-PHASE INTITATOR CC CDC18. FUNCTIONS AS A RECOGNITION FACTOR FOR RUM1 AND CDC19, WHICH CC ARE SUBSEQUENTLY UBIGUITINATED AND TARGETED TO THE 26S PROTEASOME</td><td>CC +PCW DEREMARTON. CC +1- SUBURT: BINDS TO CDC18. CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN. CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).</td><td>This betw the use modi</td></td<>	<ul> <li>267 TCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLK</li> <li>111: 111111111111111111111111111111111</li></ul>	35 38	444	<pre>Qy 495 CLQTLQGPNKHQSAYTCLQPNKNFYITSSDGTVKLWD 532   :   :      :: :::   {  :: ] Db 476 CLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILIWD 510</pre>		DT 15-JUL-1998 (Rel. 36, Created) DT 15-JUL-1998 (Rel. 36, Last sequence update) DT 01-OCT-2000 (Rel. 40, Last annotation update) DE WD-REPEAT PROTEIN POP1.	Schizose Schizose Schizose		MEDLINE-972; PubMed=9203581; Kominami K., Toda T.; Fisision yeast WD-repeat protein popl regulates genome ploidy t	did the S-phase initiator Cdc18."; (Genes Dev. 11:1548-1560(1997). [2]		CC TIC FUNCTION INVESTIGATION OF CAR INTERFACE OF FUNCTION FUNCTEADOME CC DEPENDENT DEGRADATION OF CAR INTERFOR RUM AND S-PHASE INTITATOR CC CDC18. FUNCTIONS AS A RECOGNITION FACTOR FOR RUM1 AND CDC19, WHICH CC ARE SUBSEQUENTLY UBIGUITINATED AND TARGETED TO THE 26S PROTEASOME	CC +PCW DEREMARTON. CC +1- SUBURT: BINDS TO CDC18. CC -1- SIMILARITY: CONTAINS 1 F-BOX DOMAIN. CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).	This betw the use modi

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DT 01-NOV-1995 (Rel. 32, Last sequence update) DT 01-CCT-2000 (Rel. 40, Last annotation update) DE CELL DIVISION CONTROL PROTEIN 4. GN CDC4 OR YEL009W. OS Saccharomyces cerevisiae (Baker's yeast).		rk ti SEOJUENCE FROM N.A. X MEDLINE⇔88011240; PubMed⇒3309335;					RN [3] RN [3] RP SEQUENCE OF 1-579 FROM N.A.			POLES OF THE MITOTIC SPINDLE. IT ALSO PLATS A ROLE IN BUD DEVELOPMENT, FUSION OF ZYGOTIC NUCLEI AFTER CONJUGATION AND	CC VARIOUS ASPECTS OF SPORULATION. REQUIRED FOR HTA1-HTB1 LOCUS CC TRANSCRIPTION ACTIVATION.	CC -1- SIMILARITY: CONTAINS 1 F-BOX DUMAIN. CC -1- SIMILARITY: CONTAINS 7 WD REPEATS (TRP-ASP DOMAINS).	C This SWISS-PROT entry is copyright. It is produced through a collaboration C between the Swiss institute of Bioinformatics and the EMBL outstation -	C the Buropean Bioinformatics Institute. There are no restrictions on its C use by non-profit institutions as long as its content is in no way	C modified and this statement is not removed. Usage by and for commercial c entities requires a license agreement (See http://www.isb-sib.ch/announce/	c or send an email to license@isb-sib.ch). C	0R EMBL; X05625; CAA29113.1; 28 EMBL; D50017; BAA09229.1;	NR EMBL; D46050; BAAU6499.1; R EMBL; 246255; CAAA6341.1; D DTD: D75677; D5667; D5666	R SGD; S0001885; CCC4.	DR INCEFFUS IFROUTBUSS . DR INTEFFOS IFROUTBUSS DR DFAM. DFDAGAGE F-DALO	DR PEam, PF00400; WD40; 6. DR PERMYS; PR003050; GPROTELNBRPT.	DR PROSITE; PS50181; FBOX; 1. Dr prosite; ps00678; WD_repears_1; 4.	DR PROSITE; PS50082; WD_REPEATS_2; 5. DR PROSITE; PS50294; WD_REPEATS_REGION; 1. KW Cell division: Mitosis: Socrulation: Repeat: WD repeat.	T DOMAIN 272 319 F-BOX. T REPEAT 380 408 WD 1.	FT REPEAT 420 449 WD 2. FT REPEAT 461 493 WD 3. FT PEPEAT 578 556 WD 3.	FT REPEAT 568 598 WD 5. FT REPEAT 630 658 WD 6.	FT REPEAT 669 698 WD 7. FT CONFLICT 460 460 K -> E (IN REF. 1). SQ SEQUENCE 779 AA; 86089 MW; 0348F2F8FA78F3BC CRC64;
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QY Db	249 RGELKSPKVLKGHDHVITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGH 302 1  1 1 1 1 1:::1:1:1 1 1 1 366YNPKFVPQRTTLRGHMTSVITCLQFEDNYVITGADDKMIRVYDSINKFLLQLSGH 421
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QY Db	358 SGSRDATLRVWDI
Db Db	395 RVVSGAYDFWKVWDFETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDV 450     :   :       :   :   :   :   :   :
Db Db	451 ETGNC
QY Db	<pre>491 KTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWDLKTGEFIRNLVTLESGGS 550</pre>
Db Db	551 GGVVWRIRASNTKLVCAVGSRNGTEETKLLVLDF 584 :  :       ::  ::  1   714 -DQIWSVNFKGKTLVAAV-EKDGQSFLEILDF 743
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REBEAT       1049       1079       WD 6.         REPEAT       1121       WD 9.       REPEAT       1121       WD 9.         REPEAT       1131       1121       WD 9.       REPEAT       1135       1305         REPEAT       1131       1121       WD 9.       REPEAT       1315       1305       WD 9.         REPEAT       1217       1207       WD 9.       REPEAT       1317.       Gaps         Releat       1315       FIGLOBALKM       1897.       CORSERVALCESFLITRERTVEVHORAGES       193.       Indels       137.       Gaps         1317       FIGLOBALKM       28.38.       Score 582.5.       DB 81.       Indels       137.       Gaps         1317       FIGLOBALKM       28.38.       Score 582.5.       Mismatches       193.       Indels       137.       Gaps         1317       FIGLOBALKM       28.38.       Score 582.5.       Mismatches       193.       Indels       137.       Gaps         150       Matches       19.1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1       1 <td>FТ</td> <td>REPE.</td> <td></td> <td>1007</td> <td>1037</td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td> <td></td>	FТ	REPE.		1007	1037									
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<pre>REPEAT 1217 1247 WD 10. BEQUENCE 1356 AA; 149765 MW; 965FB319844E0651 CRC64; OUMEY MAtch 18.54; Score 582.5; DB 1; Length 1356; Best Local Similarity 28.94; Pred. No. 1e-37; Matches 169; Conservative 85; Mismatches 193; Indels 137; Gaps 113 PTGLOEWLKMRELWERTVYFWQSAKPELGTASDKASNKASQEAFELVFPTGIED 649 150 PESLEEDIVKLCGSFLITRERVYFWQSAKPELGTASDKASNKASQEAFELVFPTGIED 649 150 PESLEEDIVKLCGSFLITRERVYFWQSAKPELGTASDKASNKASQEAFELVFPTGIED 649 150 PESLEEDIVKLCGSFLITRERVYFWQSAKPELGTASDKASNKASQEAFELVFPTGIED 649 150 VSYIIFWRSLNVMSQKLRRDIYCLNAPGFLIGTNVRVPDPPDPLATVRYSCIYMTHLRDLV 709 194RILAEDNLUWREKCKEEGIDEPL-HIKRK-222 710 SSTSSKWWHLLQDGDIHRFLTTKYLWLEALSLLRALPEGINAIROLESLLGHTIRGKL 769 223VIKPGFINSPWKSAYIRQHESLLGHTIRGKL 769 223VIKPGFINSPWKSAYIRQHESLLGHTIRGKL 769 223VIKPGFINSPWKSAYIRQHESLLGHTIRGKL 769 223VIKPGFINSPWKSAYIRQHESLLGHTIRGKL 769 223VIKPGFINSPWKSAYIRQHRDITN 246 770 IAIVRDGYRFALSYNMITEKAPLQAYTSALVFAPTDSMIKKIFKKEFEGWISTISVVEAE 829 247 WRRGELKSPRUKGHDHVTT-CLOFGRNYVSGSDDKTIKIMDTASGTGTGTLLGHGGS 885 306 VWSSQMRDNIIISGSTDFRLKVNANAETGSCINTLKYGHTSTVRAHLHEKRVVSGS 360 111 111 111 111 111 111 111 111 111 11</pre>	ĿЪ	REPE.		1175	1205									
<pre>BEQUENCE 1306 AA; 149705 MW; 965FB319844E0651 CRC64; DUGTY Match DUGTY Match Best Local Similarity 28.93, Score 582.5; DB 1; Length 1356; Matches 169; Conservative 85; Mismatches 193; Indels 137; Gaps 131 PTGLQEWLKM</pre>	5	REPE			247		Ч							
<pre>Duery Match 18.5%; Score 582.5; DB 1; Length 1356; Matches 169; Conservative 85; Mismatches 193; Indels 137; Gaps 113 PTGLOEWLATTON 85; Mismatches 193; Indels 137; Gaps 1150 PESLEEIVKLCGFFLIRERTVFYHOSAKDFLLGTASDKASNKASQEAFELVPFTGIED 649 150 WMOVIEPOFORDFISLLPKELALTVLSFLEPKDLLQAAOTCRYW 193 150 WMOVIEPOFORDFISLLPKELALTVLSFLEPKDLLQAAOTCRYW 193 150 WMOVIEPOFORDFISLLPKELALTVLSFLEPKDLLQAAOTCRYW 193 150 WMOVIEPOFORDFISLLPKELALTVLSFLEPKDLLQAAOTCRYW 193 150 WRULEPOFORDFISLLPKELALTVLSFLEPKDLLQAAOTCRYW 193 150 WSTIFWRSLNVMSOKLRRDITCLNADGFLIDNVRVDDPDPLATVRYSCIYWIDHLRDLV 709 194</pre>	So	SEQU			-	0		65FB31	9844EI		CRC64			
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<ul> <li>590 PESLEEIVKLCGSFLIIRERTYFFVHQSAKDFLLGTASDKASNKASQEAFELVFPTGIED</li> <li>150 MMOVIEPOFORDFISLLPKELALYVLSFLEPKDLLQAAGTCRYW</li> <li>150 MMOVIEPOFORDFISLLPKELALYVLSFLEPKDLLQAAGTCRYW</li> <li>150 MMOVIEPOFORDFISLLPKELALYULSFLEPKDLLQAAGTCRYW</li> <li>151 :: : : : : : : : : : : : : : : : : :</li></ul>	οy	113		WLKM			FOSWSG	PEKLL-		A	LDELL	DSCEPTO		4
<pre>150 MMQVIEPQFORDFISLLFKELALYVLSFLEFKDLLQAAQTCRYW 50 VSYIIFWRSLAVMSOKLRRDIYCLNAPGFLIDNVRVPDPDPLATVRYSCIYWIDHLRDLV 194RILAEDNLLMREKCKEEGIDEPLHIKRKF- 710 SSTSSKWVHLLQDDGDIHRFLTFKVLYMLEALSLLRALPEGINAIRQLESLLGHTIRGRL 223 -VIRDGFRILAEDNLLMRERCKEEGINAIRQLESLLGHTIRGRL 223 -VIRDGFRILAEDNLLMREIDTN 770 IAIVRDGFFALSTRMIIEKAPLQAYTSALVFAPTDSMTKYWRAVTGRRIDTN 770 IAIVRDGFFALSTRMIIEKAPLQAYTSALVFAPTDSMTKYWSAVTGQHCIDTN 770 IAIVRDGFFALSTRMIIEKAPLQAYTSALVFAPTDSMTKYWSAVTGQHCIDTN 770 IAIVRDGFFALSTRMIIEKAPLQAYTSALVFAPTDSMTKYWSAVTGQHSIDTN 780 MWS</pre>	ą	590		:   : IVKLCG	SFLIIR	RERTVY	 FVHQSA	:    KDFLLG	TASDKI	ASNKA.	l SQEAF	:    ELVFPTG		49
<ul> <li>550 'SYIIFWRSLAVMSOKLRRDIYCLNAPGFLIDNVRVPDPDPLATVRYSCIYWIDHLRDLV</li> <li>194RILAEDNLLMREKCKEBGIDEDLHIKRK-</li> <li>710 SSTSSKWVHLLQDDGDIHRFLTKKYLWLEALSLLRALPEGINAIRQLESLLGHTIRGRL</li> <li>223 -VIKDGFRILAEDNLLMREKCKEBGINAIRQLESLLGHTIRGRL</li> <li>223 -VIKDGF FALSYRMIIEKAPLQAYTSALVFAPDSMIKIFKFEPGUNAIRQHEGRL</li> <li>224 WRGEKSFKLKGHDDHYT-CLOFGGNRIYSGSDDNTLKVWSAVTGOHRG-</li> <li>247 WRGEKSFKLKGHDDHYT-CLOFGGNRIYSGSDDNTLKVWSAVTGOHRGG</li> <li>248 WSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSGHGGS</li> <li>306 WSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSGHGGSVGSSDDRTLKWWSAVFBDFGGGNGS</li> <li>316 WSSQMRDNIIISGSTDRTLKVWNAETGECIHTLYGHTSGHGGS</li> <li>317 NIACTQTLEGHGSSVLSVASGSDGRTIKIMDTASGTCTQTLEGHGGRVOSGSDGRVASGSDDRTLKVWDPETETCHT</li> <li>318 WSVAFSPDRER-VASGSDDRTLKVWNAETGECIHTLYGHTSTVRMHLHEKRVVSGS</li> <li>318 WSVAFSPDRER-VASGSDDRTLKVWNAETGECIHTLYGHTSTVRMHLHEKRVVGSGS</li> <li>318 WSVAFSPDRER-VASGSDDRTLKVWNAETGECIHTLYGHTSTVRMHLHEKRVVSGS</li> <li>318 WSVAFSPDRER-VASGSDDRTLKVWNAETGECIHTLYGHTSTVRMHLHEKRVVSGS</li> <li>321 RDATLRVWDFETGCLHVLMGHVAAVRCVYDGRRVVSGAYDFWVKWDPETETCHT</li> <li>321 RDATLRVWDFETGGCLHVLMGHVAAVRCVYDGRRVVSGAYDFWVKWDPETETCHT</li> <li>321 RDATLRVWDFETGGSCLHVLMGHVAAVRCVYDGRRVVSGAYDFWVKWDPETETCHT</li> </ul>	ò	150		VOM	IEPOFO	RDFIS	LLPKEL	AL'YVI.S	FLEPKI	PL LOA	AOTOR		:	50
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	4,5 Compugen Ltd.		<pre>Search time 22.58 Se (without alignments) 3451.181 Million cell</pre>	. SRNGTEETKLLVLDFDVDMK			satisfying chosen parameters: 425026			,			results predicted by chance to have I to the score of the result being pr of the total score distribution.		Descr	Q9nu: Q9vz: 04401	09921 0921	099u 09r1 04438	0907v1 09p7v1 096611	60 0 60 0 60 60	160 160 160

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<pre>Heiman T.J., Hernandez J.R., Houck J., Hevland T.J., Wei MH., Ibegwam C., Hovland T.J., Wei MH., Ibegwam C., Karpen G.H., Ke Z., Kennison J., Kethum D., Kraft C., Kravitz S., Kulp D., Lai Z., Itosh T.C., McLeod M.P., McPherson D., 4.V., Mobarry C., Morshir S.J., Mesher P.P., Nazary D.M., Nelson D.L. P., Nixon K., Nusskern D.R., Pacleb J.M. S.S., Pan S., Pollard J., Puri V., Reese M C., Saunders R.D.C., Scheeler F., Shen H., S. Stapleon M., Skupski M.P., Smith T., T.Y. Stappon M., Strong R., Sun E., Turner R., Venter E., Wang A.H., Wang X. J.S., Pan S.Crong G.M., Weissenbach J., T., Nariey K.C., Wu D., Yang S., Yao Q.A. T., Shou X., Zhuu S., Zhu X., Smith R. Dosophila melanogaster.", Rubin G.M., Venter J.C., Rubin G.M., Kenter J.C., Rubin G.M., Kenter J</pre>	; AAG22246. 035516; CG1 01680; 01810; WD40; 7. F-box; 1. 0; CPROTEIN 0; CPROTEIN 81; FBOX; 1. 78; WD_REPE eat. 6 AA; 1413	uery Match 65.6%; Score 2062.5; DB 5; Length 1326; lest Local Similarity 66.8%; Pred. No. 1.8e-166; latches 405; Conservative 54; Mismatches 98; Indels 49; Ga	12 GLVPVDLKSAKEPLPHQTVMKIFSISIIAQGLPFCRRRMKR     : :       : :       : :   :   :   :	53 KLDHGSEVRSFS-LGKKPCKVSEYTSTTGLVPCSATPTFGDLRAANGQGQQRRRITSV- 	<pre>111OPPTGLOEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLP 11 11 11 11 11 11 11 11 111111111111</pre>	<pre>168 KELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEGIDEPLHIKRR 1111:111:1111111:1111111111111111111</pre>	<pre>222 KVIKPGFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHDDHVITCLQFCGNRIVSGSD : 1                                    </pre>	282 DNTLKVWSAVTGKCLRTLVGHTGGVWSSQMRDNIIISGSTDRTLKVWNAETGECIHTLXG 111111111111111111111111111111111111	342 HTSTVRCMHLHEKRVVSGSRDATLRVWDIETGQCLHVLMGHVAAVRCVQYDGRRVVSGAY 111111111111111111111111111111111111	402 DFMVKVWDPETETCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLG 1:111:1 1:1 1:111111111111111111111111	462 HQSLTSGMELKDNILVSGNADSTVKIMDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVIT 
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372 ATLHGHHAAVRCVQFDGTTVVSGGYDFTVKIWNAHTGRCIRTLTGHNNRVYSLLFESERS 431 ::|: | | : : || |: : 0 QHWKKLIEKNVRSDSLWWGLSEKRQWDKFLNISRDMSVRRICEKFNYD--VNIKRDKLDQ 179 SATPTTFGDLRAANGQGQQRR--RITSVQPPTGL-QEWLKMFQSWSGPEKLLALDELIDS 141 458 TLTGHQSLTSGMELKDNILVSGNADSTVKIWDIKTGQ------CLQTLQGPNKHQSA 508 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis. NCBL\_TaxID=6239; 
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Db       427       NGHRRGIACLQYRDRLVVSGSSDNTIRLWDIEGGACLRVLEGHEELVRCIRFDNKRIVSG       486         Qy       480       NADSTVKIWDIKTGQCLQTLQGPNKHOSAVTCLQFNKNEVTSSDDGTVKL       530         Qy       480       NADSTVKIMDIKTGQCLQTLQGPNKHOSAVTCLQFNKNEVTSSDDGTVKL       530         Qy       480       NADSTVKIMDIKTGQCLQTLQGPNKHOSAVTCLQFNKNEVTSSDDGTVKL       530         Qy       487       AVDGKIKVWDLMAALDPRAPAGTLCLRTLVEHSGRVFRLQFDEFQIVSSSHDDTILI       543         Qy       531       WD       532         Db       544       WD       545	RESULT 6 09QUI5 PRELIMINARY; PRT; 569 AA. DC 09QUI5 PRELIMINARY; PRT; 569 AA. AC 09QUI5; DT 01-MAY-2000 (TrEMBLrel. 13, Created) DT 01-MAY-2001 (TREMBLrel. 14, Last sequence update) DT 01-MAY-2001 (TREMBLrel. 16, Last annotation update) DE UBIOUTTIN LIGASS FWD1. OS Mus musculus (Mouse). OC BUARTYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NISL_TAXID=10090;	<pre>RP SEQUENCE FROM N.A. RX MEDLINE=99199275; PubMed=10097128; RX MEDLINE=99199275; PubMed=10097128; RA Hattori K., Higashi H., Nakano H., Okumura K., Once K., Good R.A., RA Hattori K. Higashi H., Nakano H., Okumura K., Once K., Good R.A., RA Ubiquitin-dependent degradation of IkappaBalpha is mediated by a RT "Ubiquitin ligese skpl/Cull JFPox protein FWD1."; Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999). RL Proc. Natl. Acad. Sci. U.S.A. 96:3859-3863(1999). R SEQUENCE FROM N.A. RX MEDLINE=99075339; PubMed=9859996; RA MADLINE=99075339; PubMed=9859996; RA Taron A., Hattubai A., Davis M., Lavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Lavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Lavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon I., Amit S., Manning A.M., RA Taron A., Hattubai A., Davis M., Eavon A., Hattubai A., Davis M., Manukai A., Manukai A., Matubai A., Davis M., Eavon A., Hattubai A., Davis M., Marcurio F., Ben-Neriah Y.;</pre>		Query Match20.2%; Score 635; DB 11; Length 569;Best Local Similarity30.3%; Pred. No. 1.3e-45;Matches164;Conservative92; MismatchesQy53 KLDHGSEVRSFLGKKPCKVSEYTSTGLVPCSATPTFGDLQy53 KLDHGSEVRSFLGKKPCKVSEYTSTGLVPCSATPTFGDLQy53 KLDHGSEVRSFLGKKPCKVSEYTSTGLVPCSATPTFGDLQy53 KLANGGGQGRRIFSVOPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHQy95 RAANGQGQGRRIFSVOPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHQy95 RAANGQGQGRRIFSVOPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHQy95 RAANGQGQGRRIFSVOPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHQy95 RAANGQGQGRRIFSVOPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHQy95 RAANGQGQGRRIFSVOPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHQy95 RAANGQGQGRRIFSSSYEKELCVKYFEQWSESDQVEFVEHLISOMCHYOHGHQy111:13111:14:11:15:111:16:11:17:11:17:11:18:11:19:11:19:11:19:11:10:11:11:11:11:11:12:11:13:11:13:11:14:11:15:11:16:11:17:11:18:11:19:11:19:11:10:11:10:11:11:11:11:11
4 20 VLEGHE 509 VTCLQF 509 VTCLQF 477 VFRLQF 2159 202159 092159	AC 092139; DT 01-MAY-1999 (TrEMBLrel. 10, Created) DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DE BETA-TRANSDUCIN REPEAT CONTAINING PROTEIN. DE BETA-TRANSDUCIN REPEAT CONTAINING PROTEIN. OS Mus musculus (Mouse). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; OC Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxtD=10090; RI [1] RP SEOUENCE FROM N.A. RX MEDLINE-99145465; PubMed=9990853; RA SPENCER E, Jiang J., ChanaBloha hu tho E-how montain "Scincal-Induced and Montification.	SIIMb/DEEn-TCEP."; June 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1. 1.	Query Match20.2%; Score 635; DB 11; Length 569;Best Local Similarity30.3%; Pred. No. 1.3e-45;Matches 164; Conservative 92; Mismatches 214; Indels 72; Gaps 14;Qy53 KLDHGSEVRSFSLGKKPCKVSEYTSTTGLVPCSATPTTFGDL 94I1	<pre>Db 132 INSYLKFWLORDFITALPARGLDHIAENILSYLDAKSLCAEELVCKEWYRYTSDGMLWKK 191 QY 206 KCKEEGIDEPLHIKRKKVIKPGFIHSPWKSAYIRQ-HRI 243 Db 192 LIERWNRTDSLWRGLAERRGWGYLFKNKPPDENAPENSFYRALYPKIIQDIETI 246 QY 244 DTWNRRGELKSPKV-LKGHDDHVITCLQFCGNRIYSGSDDNTLKWWSYTGKCLRTLVGH 302 247 ESNWRCGRHSLQRTHCRSETSKGVYCLQYDDQKIVSGLRDNTIKIWDKSTLECKRILTGH 306 QY 303 TGGVWSSQMRDNII1SGSTDRTLKVWAAETGECIHTLYGHTSTVRMMKSTLECKRILTGH 306 QY 303 TGGVWSSQMRDNII1SGSTDRTLKVWANAETGECIHTLYGHTSTVRMMLHEKRVVSGSBD 362 D1 11 1 111111 1111 111 111 111 1111 1</pre>

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Db1921:111 <th>Qy       420       0GHTNRVYSLQFDCIHVVSGSLDTSIRVWDVETGNCIHTLFGHOSLTSGMELKDNILVSG       479         1       1       1       1       1       1       1         1</th> <th>Db 544 WD 545 RESULT 8 044382 044382 PRELIMINARY; PRT; 510 AA. AC 044382; PRELIMINARY; PRT; 510 AA. DT 01-JUN-1998 (TERMELTE1. 06, Created) DT 01-JUN-1998 (TERMELTE1. 06, Created) DT 01-MAR-2018 (TERMELTE1. 06, Last sequence update)</th> <th>B OR CG3412. B OR CG3412. elanogaster (Fru eeptera, Endopte Drosophilidae; 227;</th> <th></th> <th></th> <th>Query Match 19.6%; Score 617; DB 5; Length 510; Best Local Similarity 30.6%; Pred. No. 3.9e-44; Matches 146; Conservative 91; Mismatches 190; Indels 50; Gaps Out 104 DEDImentoDensioner Verocesconservations 152</th> <th><ul> <li>1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1</li></ul></th>	Qy       420       0GHTNRVYSLQFDCIHVVSGSLDTSIRVWDVETGNCIHTLFGHOSLTSGMELKDNILVSG       479         1       1       1       1       1       1       1         1	Db 544 WD 545 RESULT 8 044382 044382 PRELIMINARY; PRT; 510 AA. AC 044382; PRELIMINARY; PRT; 510 AA. DT 01-JUN-1998 (TERMELTE1. 06, Created) DT 01-JUN-1998 (TERMELTE1. 06, Created) DT 01-MAR-2018 (TERMELTE1. 06, Last sequence update)	B OR CG3412. B OR CG3412. elanogaster (Fru eeptera, Endopte Drosophilidae; 227;			Query Match 19.6%; Score 617; DB 5; Length 510; Best Local Similarity 30.6%; Pred. No. 3.9e-44; Matches 146; Conservative 91; Mismatches 190; Indels 50; Gaps Out 104 DEDImentoDensioner Verocesconservations 152	<ul> <li>1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1</li></ul>
Db 192 LIERMVRTDSLWRGLAERRGWGQYLFKNKPPDENAPPNSFYRALYPKIIQDIETI 246 OY 244 DTNMMRGELKSPKV-LKGHDDHVITCLOFCGNRLVSGSDDNTLKVWSAVTGKCLRTLVGH 302 1:111 ::::::::::::::::::::::::::::::::	48 53 54	SUL	<pre>OS Mus musculus (Mouse). OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. OX NCBI_TAXID=1090; RN [1] RP SEQUENCE FROM N.A. RA Winston J., Elledge S.J., Harper J.W.; RA Winston J., Elledge S.J., Harper J.W.; R1 Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.</pre>	EMBL; AFI10306; ADD InterPro; IPR001680, InterPro; IPR001800, Pfam; PF00400; WD40, Pfam; PF00646; F-boo PRINTS; PR00320, GPP PR0SITE; PS50181; FI PR0SITE; PS50181; FI PR0SITE; PS00300; W140, PR0SITE; PS00300; W140, PS00300; W140, PS00	Query Ma Best Loc Matches 53	<pre>Db 14 KFMNSSEREDCNNGEPPRKIIPEKNSLRQTYNSCARLCINQETVCLTSTAMKTENCVAKA 73 QY 95 RAANGQGQORRRITSVQPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKH 149</pre>	<pre>150 MMOVIEPOFORDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE 150 MMOVIEPOFORDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWRE 132 INSYLKPMLQRDFITALPARGLDHITENILSYLDAKSLCAAELVCKEWYRVTSDGMLWKK 206 KCKEEGIDEPLHIKRKVIKPGFIHSPWKSAYIRQHRI</pre>

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<pre>RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X RA Wang XY., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., RA T.J., Yeh RF., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhang L., RA Clibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RA Clibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RA Clibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RA Clibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; R. Cleance 287:2185-2195(2000). RI Science 287:2195(2000). RI Science 287:2195(2000). RI S</pre>	<pre>EFINTS: PFO03.5: F-Dox: 1. EFINTS: PFO03.5: F-Dox: 1. PFONTS: PFO03.5: PFO03.</pre>
<ul> <li>QY 216 LHIKRKVIKPGFIHSPWKSAYIRQHRIDTNWRGELKSPKV-LK 259</li> <li>Db 150 L-AERRNWMQYLFKPRGQTQRPHSFHRELFPKIMNDIDSIENNWRTGRHMLRRINCR 206</li> <li>QY 260 GHDDHVITCLQFGGNRIVSGSDDNTLKVWSAYTGKCLRTLVGHTGGVWSSQMRDNIIISG 319</li> <li>::!!!:!!:!!!:!!!!!!!!!!!!!!!!!!!!!!!!</li></ul>	<pre>RESULT 9 GVDB3 RELINIANT: PT: 510 A. GVDB3 RELINIANT: PT: 510 A. GVDB3 RELINIANT: PT: 510 A. GVDB3 RELINIANT: FORTER: 13, Created) C GVART-2000 (TERMILTE1 15, Last sequence update) SIAB OR CG311.MB3 C GVART-2000 (TERMILTE1 15, Last sequence update) C GVART-2000 (TERMILTE1 15, Last sequence update) C GVART-2000 (TERMILTE1 15, Last sequence update) C GVART-2000 (TERMILTE1 16, Last annotetion update) C GVART-2000 (TERMILTE1 16, Last annotetion update) C C FART-2010 (TERMILTE1 16, Last annotetion update) C FART-2010 (TERMILTE1 16, Last annotetion (TERMILTE1 10, TERMILTE1 10,</pre>

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14; 55 DHGSEVRSFSLGKKPCKVSEYT - - - - STTGLVPCSATPTTFGDLRAANGQGQQRRRITS 109 110 VOPPTGLQEWLKMFQSWSGPEKLLALDELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKE 169 216 80 VSLRVFSYLDQLDLCKCKLMSKRWKRLLEDPGIWKALYMQKGWFVNENVLNEFEAWRRTH 139 251 140 KFPQPRFENFLKQQNIIGPYGTMFLPQQFIFDSNGRPLLNWSYLYKEHAHLDSNWRHGRF 199 301 259 359 319 413 

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 <t 473 439 533 EKIVSGGYDGTVRIWNFWTGEQHCVLH--NSRNSRVFGLQFDHRRIIACTHSSEILVWWF 497 79 Gaps 5 DNGKNVVS-------KVSDLTSCSDFSTSSPVPC------LNPLSHENNRIDL 44 г. 

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 HSGSVLCLDFCRRNLLVSGSSDSTIIINDMQNRRPLKYYFGHTDNVLGVVVSENYIISS

 45 IR---------DLLASLSKEGVVAVYNHVRSLLFTDFTEVFPEE 170 LALYVLSFLEPKDLLQAAQTCRYWRILAEDNLLWREKCKEEG--IDEPL-----------LKSPKVLKGHDDHV-----ITCLQFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVG 200 LVSTFNNPSIRFPADQDFRATLDSVYCVQYDDEIMVSGSKDRTVSVWDVNSRFILYKLYG HTGGVWSSQM--RDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLHEKRVVSG SRDATLRVWDIETGQ----CLHVLMGHVAAVRCVQYDGRR--VVSGAYDFMVKVWDFETE TCLHTLQGHTNRVYSLQFDGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQSLTSGMELKD NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSSDDGTVKLWDL ------HIKRRKVIKP-GFIHSP------WKSAYIRQHRIDTNWRRGE-MCDOUGall R.C., Rajandream M.A., Barrell B.G., Brown S., Murphy Jones L., McNeil A., Harris D.; Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases. EMBL, All36539; CAB6464.1; -. InterPro; IPR001680; -. InterPro; IPR001680; -. Pfam; PF00646; F-box; 1. Indels 108; Length 506; CEF34D4EFFBC2E10 CRC64; Schizosaccharomyces pombe (Fission yeast). Eukaryota: Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetales; Schizosaccharomycetaceae; Schizosaccharomyces. Last sequence update) Last annotation update) 17.0%; Score 533; DB 3; L4 25.8%; Pred. No. 5.4e-37; tive 91; Mismatches 204; 506 AA PRINTS; PR00320; GFROTEINBRPT. PROSITE; PS50181; FBOX; 1. PROSITE; PS00578; WD\_REPEATS; UNKNOWN\_3. Created) PRT ; •• 58256 MW; 01-077-2000 (TrEMBLrel. 15, 01-077-2000 (TrEMBLrel. 15, 01-MAR-2001 (TrEMBLrel. 16, Query Match 17.0%; Best Local Similarity 25.8%; Matches 140; Conservative PRELIMINARY; SMART; SM0256; FBOX; 1. Repeat; WD repeat. 506 AA; WD-REPEAT PROTEIN. SEQUENCE FROM N.A. NCBI\_TaxID=4896 **KTG 536** STRAIN=972H SPAC30.05 SEQUENCE 29P7V1: **IV7460** 252 320 380 440 534 217 302 360 414 474 q đ ą g 20 20 g Q g δ δ δ Q g Q q δ ą š

18; 446 TLSTNFTNTTATTTTN--ATNSNINQQQQQQQQQQPPTRTQR-VSISAGSSNNKRYTPP 502 195 503 ISTSTSSSSSSILNNFSI------NILLPINLILLIFREIKPNFVNTLSRVCKHWKQ 553 362 254 554 IIDDDELWNKYCSD-------RLINKSKFEESITWKSNYIKIYKQQKWFHNKL-N 601 255 PKVLKGHDHVITCLQFCGNR - - IVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVWSSQMR 312 657 

 SGLNIINNNSNNSNSSSSNSSSSNSRYLFSLKGHSGCIKSVDYQRQSGSDVSRVFTASAD
 717

 ATLRVWDIETGQCLHVLMGHVAAVRCVQYDG - - - RRVVSGAYDFMVKVWDPETETCLHTL 419 Gaps 76 TSTTGLVPCSATPTTFGDLRAANGQGQQRRRITSVQPPTGLQEWLKMFQSWSGPEKLLAL 135 Chung C.Y., Reddy T.B.K., Zhou K., Firtel R.A.; "A novel, putative MEK kinase controls developmental timing and spatial patterning in Dicryostellum and is regulated by ubiguitin-mediated protein degradation."; Genes Dev. 12:3544-3578(1998). -1- SIMILARITY: TO THE SER/THR FAMILY OF PROTBIN KINASES. EMBL; AF093689; AAC97114.1; -. InterPro; IPR001245; -. InterPro; IPR001245; -. LAEDNLLWREKCKEEGIDEPLHIKRRKVIKPGFIHS - PWKSAYIRQHRIDTNWRRGELKS HSTLKGHDKGVF-CVKLIDDQGMVLSGGEDKKLKVWD-ISGNHHN--HHSGIVGSISKK D - - NIIISGSTDRTLKVWNAETGEC - - IHTLYGHTSTVRCMHLHEK - - - - - - RVVSGSRD 136 DELIDSCEPTQVKHMMQVIEPQFQRDFISLLPKELALYVLSFLEPKDLLQAAQTCRYWRI 59; ATP-binding; Kinase; Repeat; Serine/threonine-protein kinase; Transferase; Tyrosine-protein kinase; WD repeat. SEQUENCE 942 AA; 105796 MW; C9E4928A8C7C68F7 CRC64; Length 942; .. Indels Dictyostelium discoideum (Slime mold). Eukaryota; Mycetozoa; Dictyostelium. Last sequence update) Last annotation update) Query Match 14.7%; Score 463.5; DB 5; Best Local Similarity 24.6%; Pred. No. 1e-30; Matches 127; Conservative 118; Mismatches 212; A 942 PROSITE; PS50181; FBOX; 1. PROSITE; PS50107; PROTEIN\_KINASE\_ATP; 1. PROSITE; PS500107; PROTEIN\_KINASE\_DOM; 1. PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1. PROSITE; PS00678; WD\_REPEATS; UNKNOWN\_4. Created) PRT; MEDLINE=99051319; PubMed=9832508; Pfam; PF00646; F-box; 1. PRINUS; PR00320; GPROTEINBRPT. PRINUS; PR00130; TURNIASE. PRINUS; PR00109; TURNIASE. PROSITE; PS00107; PROTEIN\_KINA! ) (TrEMBLrel. 10, ( (TrEMBLrel. 10, 1) (TrEMBLrel. 16, 1 InterPro; IPR002290; -. Pfam; PF00069; pkinase; 1. PRELIMINARY; 01-MAY-1999 (TrEMBLrel. Pfam; PF00400; WD40; 7. InterPro; IPR001810; -. SMART; SM00320; WD40; SEQUENCE FROM N.A. NCB1\_TaxID=44689; MEK KINASE ALPHA. 500 STRAIN=KAX-3 01-MAY-1999 01-MAR-2001 DDC 096611 096611 11 498 658 MKKA. 196 602 313 363 RESULT 096611 ß ą đ đ q g S δ  $\Omega$ ą δ 20 δ

RESULT 13 Q9PTR5 ID Q9PTR5 RELIMINARY; PRT; 410 AA. 09PTR5; PRELIMINARY; PRT; 410 AA. PT 01-MAY-2000 (TrEMBLrel. 13, Created) PT 01-MAY-2001 (TrEMBLrel. 15, Last sequence update) PT 01-MAY-2001 (TrEMBLrel. 15, Last sequence update) PT 01-MAY-2001 (TrEMBLrel. 16, Last annotation update) CO 01-MAY-2001 (TrEMBLrel. 16, Last annotation update) C 2010 (TREM	OX NCBL_TaxID=9031; RN [1] RP SEQUENCE FROM N.A. Reiner O., Shmueli O.; RT "Characterization of the chicken homolog of LIS1."; RL Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. DR InterPro: IFR001680; DR PRINFTS; PR001680; DR PRINFTS; PR00120; GPROTEINBRPT. DR PRINFTS; PR00320; GPROTEINBRPT. DR PRINFTS; PR00320; GPROTEINBRPT. DR RINFTS; PR00320; GPROTEINBRPT. DR REPEAT; MD TEPEATS; UNKNOWN_5. SEQUENCE 410 AA, 46664 MW; FC5848D06E0DCA20 CRC64;	Query Match14.0%;Score 439;DB 13;Length 410;Best Local Similarity29.9%;Pred. No. 4e-29;Matches109;Conservative63;Mismatches133;Indels60;GapsQy227GFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHD263;Mismatches133;Indels60;GapsQy227GFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHD263;Mismatches133;Indels60;GapsQy227GFIHSPWKSAYIRQHRIDTNWRRGELKSPKVLKGHD263;Mismatches161;111Db49GLLEKKWTSVIRLERSKLNEAKEEFTSGGPLGCKRDFKEWIPRPEKYALSGHR108203263DHVITCL-OPCGNRLVKSGSDDNTLKVWSAVGKLERTLVGHTGGWWSSQMRDNIIISG319Qy263DHVITCL-OPCGNRLVKSGSDDNTLKVWDFFFGGFFERTLKGHTDSVQDISFDHTGKLLASC16811 <th>Db 169 SADMTIKLWDFOGFECIRTMHGHDHNVSSVAIMPNGDHIVSASRDKTIKMWEVOTGYCVK 228 QY 378 VLMGHVAAVRCQYDGRRVVSGAYDFMVKWMPETETCLHTLQGHTNRVYSLQF 431 1 11 1; 1 1 1; 1 4; 1 11 1; 1 1 229 TFTGHREWVRMVRPNQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPES 288 QY 432DGHLVVSGSLDTSIRVMDVETGNCIHTLTGHQSLTSGMELKB 473 Db 289 SYSTISEATGSETKKSGKP6FLLSGSRDKTIKMMDISTGMCLMTLVGHDNWVRGVLFHS 348 OV 474NITVSCNADSTURINDTKTCOCTOFDNKHOSENVCTORN</th> <th>349 GGKFILSCADDKTLRVWDFKNKRCMKTLNAHEHFVTSLDFHKTAPYVVTGSVDQTVK 530 LWDLK 534 : : : 406 VWECR 410</th> <th>09GLD-1 ID 09GL51 PRELIMINARY; PRT; 410 AA. AC 09GL51; PRELIMINARY; PRT; 410 AA. DT 01-MAR-2001 (TrEMBLrel. 16, Created) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) C 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TR</th>	Db 169 SADMTIKLWDFOGFECIRTMHGHDHNVSSVAIMPNGDHIVSASRDKTIKMWEVOTGYCVK 228 QY 378 VLMGHVAAVRCQYDGRRVVSGAYDFMVKWMPETETCLHTLQGHTNRVYSLQF 431 1 11 1; 1 1 1; 1 4; 1 11 1; 1 1 229 TFTGHREWVRMVRPNQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPES 288 QY 432DGHLVVSGSLDTSIRVMDVETGNCIHTLTGHQSLTSGMELKB 473 Db 289 SYSTISEATGSETKKSGKP6FLLSGSRDKTIKMMDISTGMCLMTLVGHDNWVRGVLFHS 348 OV 474NITVSCNADSTURINDTKTCOCTOFDNKHOSENVCTORN	349 GGKFILSCADDKTLRVWDFKNKRCMKTLNAHEHFVTSLDFHKTAPYVVTGSVDQTVK 530 LWDLK 534 : : : 406 VWECR 410	09GLD-1 ID 09GL51 PRELIMINARY; PRT; 410 AA. AC 09GL51; PRELIMINARY; PRT; 410 AA. DT 01-MAR-2001 (TrEMBLrel. 16, Created) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) C 01-MAR-2001 (TrEMBLrel. 16, Last sequence update) DT 01-MAR-2001 (TR
<pre>Db 718 FTCKIFSLKTKFLETYTNHQEAVTCINYLGDVENKCITSSLDKTIQLWDAETGSCLSTL 777 Qy 420 QGHTNRVYSLQFDGIH-VVSGSLDTSIRVWDVETGNCIHTLTGHOSLTSGME 470 11   i  i  i  i  i  i  i  i  i  i  i  i  i</pre>	RESULT 12 09NWX7 PRELIMINARY; PRT; 334 AA. D 09NWX7; PRELIMINARY; PRT; 334 AA. AC 09NWX7; DT 01-OCT-2000 (TEMBLrel: 15, Last sequence update) DT 01-OCT-2001 (TEMBLrel: 15, Last sequence update) DT 01-MAR-2001 (TEMBLrel: 16, Last annotation update) DT 01-MAR-2001 (TEMBLrel: 16, Last annotation update) DT 01-MAR-2001 (TEMBLrel: 15, Last annotation update) DT 01-MAR-2005 (		Query Match14.7%; Score 461; DB 4; Length 334;Best Local Similarity33.9%; Pred: No. 4e-31;Best Local Similarity33.9%; Pred: No. 4e-31;Matches 102; Conservative 68; Mismatches 93; Indels 38; Gaps 13;Qy258 LKGHDHVITCLOFCGRIVSGSDNTLKVWSAVTGKCLRTUGHTGGVWSSQM 311	<pre>Db 99 -SMLLVSASDDFTLKTMPVSSGKCLKTLKGHSNYVFCCNENPQSNLIVSGEFDESVRIWD 157 Qy 370 IETGQCLHVLMGHVAAVRCVQY - DGRRVVSGSYDFMVKWDDETETCLHTLQGHTNRVY 427 i:  :                 1   1   1   1   1  </pre>	QY 475 ILVSGNADSTVKIWDIKFGQCLQFLQGENKHQSAVTCLQFNKNFVITSSDDGTVKL 530 1111:1:111:1:1111 Db 273 WIVSGSEDNLVYIWNLQTKEIVQKLQGHTDVVISTACHPTENIIASAALENDKTIKL 329 QY 531 W 531 Db 330 W 330

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  SEQUENCE FROM N.A.
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  Nagasaka T., Boulday G., Coupel S., Coulon F., Tesson L.,
  Nagasaka T., Soulillou J.-P., Charreau B.;
  "Cloning of porcine PAF-AH Ib-alpha CDNA and expression in endothelial
  "Cloning of porcine PAF-AH Ib-alpha CDNA."" Astahases.
- Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF319658; AAG33867.1; -. Hydrolase. 410 Aa; 46554 MW; A08DAFCDB8BB2719 CRC64; SEQUENCE 410 AA; 46554 MW; A08DAFCDB8BB2719 CRC64; SO REAR RAN COC SO COC
- 410 AA; 46654 MW; A08DAFCD8B8B2719 CRC64;

263 DHVITCL-QFCGNRIVSGSDDNTLKVWSAVTGKCLRTLVGHTGGVW--SSQMRDNIIISG 319 288 49 GLLEKKWTSVIRLOKKVMELESKLNEAKEEFTSGGPLGQKRDPKEWIPRPEKYALSGHR 108 109 SPVTRVIFHPVFSVMVSASEDATIKVWDYETGDFERTLKGHTDSVQDISFDHSGKLLASC 168 377 378 VLMGHVAAVRCVQ--YDGRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVYSLQF---- 431 60; Gaps 320 STDRTLKVWNAETGECIHTLYGHTSTVRCMHL--HEKRVVSGSRDATLRVWDIETGQCLH 229 TFTGHREWVRMVRPNQDGTLIASCSNDQTVRVWVVATKECKAELREHEHVVECISWAPES 13.9%; Score 436; DB 6; Length 410; 29.9%; Pred. No. 7.1e-29; 63; Mismatches 133; Indels Best Local Similarity 29.9 Matches 109; Conservative Query Match 169 ą ą đ 20 ð 5 g δ

- 473 432 S
- 289 SYSSISEATGSETKKSGKPGPFLLSGSRDKTIKWWDVSTGMCLMTLVGHDNWVRGVLFHS 348 g
- 529 - - NILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKN - - FVITSSDDGTVK 474 δ
  - 405 ::| | |:::|| | :::|| | ::|| | :|: || |:| :|:| | |:| 349 GGKFILSCADDKTLRVWDYKNKRCMKTL---NAHEHFVTSLDFHKTAPYVVTGSVDQTVK g
- 530 LWDLK 534 δ
- :|: : 406 VWECR 410 q
- RESULT 15
  - Q9NUL4
- 330 AA. PRT; PRELIMINARY; Q9NUL4; Q9NUL4

- 01-02T-2000 (TEBBLrel. 15, Created) 01-02T-2000 (TEBBLrel. 15, Last sequence update) 01-MAR-2001 (TEBBLrel. 15, Last annotation update) 01-MAR-2001 (TEBBLrel. 16, Last annotation update) INCOMPATIBILITY PROTEIN HET-E-1.
  - Homo sapiens (Human).
- Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  - NCBI\_TaxID=9606,
- TISSUE-PLACENTA,

- EMBL; AK002149; BAA92110.1; -.
- Isoogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y., Isobata T., Nagai K., Sugano S., Shiratori A., Sudo H., Sugawara M., Wagatsuma M., Hosolri T., Kaku Y., Konda H., Kondo H., Sugawara M., Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S., Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Minomiya K., Iwayanagi T., Nakamura Y., Nagahari K., Masuho Y., "NEDO human CDNA Sequencing project."; Submitted (FP-2000) to the EMBL/Genbank/DDBJ databases.

: ::| | |:|||:|: :|:|| ||:: | | :: :::||| | :::!: 95 -SSRLVSASDDKTLKLMDVRSGKCLKTLKGHSNYVFCCNFNPPSNLLISGSFDETVKIME 153 154 VKTGKCLKTLSAHSDPVSAVHPNCSGSLIVSGSYDGLCRIWDAASGQCLKTLVDDDNPPV 213 312 RDNIIISGSTDRTLKVWNAETGECIHTLYGHTSTVRCMHLH--EKRVVSGSRDATLRVWD 369 370 IETGQCLHVLMGHVAAVRCVQYD - - GRRVVSGAYDFMVKVWDPETETCLHTLQGHTNRVY 427 258 LKGHDDHVITCLQFC--GNRIVSGSDDNTLKVWSAVTGKCLRTLVGH----TGGVWSSQM 311 
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 LVGHTE-AVSSVKFSPNGEWLASSSADRLIIIMGAYDGKYEKTLYGHNLEISDVAWSSD-94
 S-LQF--DGIHVVSGSLDTSIRVWDVETGNCIHTLTGHQ-----Query Match 13.6%; Score 426; DB 4; Best Local Similarity 31.8%; Pred. No. 3.7e-28; Matches 95; Conservative 71; Mismatches 99 428 q q q q 2 δ 5 S 10;

12;

Gaps

34;

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Length 330; Indels

F78396D3B5B716CA CRC64;

InterPro; IPR001632; -. InterPro; IPR001680; -. Pfam; PF00400; WND; 7. PRINTS; PR00319; GPROTEINB. PRINTS; PR00320; GPROTEINBRPT. PR051TE; PS00678; WD\_REPEATS; UNKNOWN\_4. Repeat. WD repeat. SEQUENCE 330 AA; 36329 MW; F78396D3B5B7

- ---SLTSGMELKDN 474 531 475 ILVSGNADSTVKIWDIKTGQCLQTLQGPNKHQSAVTCLQFNKNFVITSS--DDGTVKLW δ
  - :|||: |: | ||:::| :: | ||| : | :| ::: :| |:||] 269 WIVSGSEDNLVYIWNLQTKEIVQKLQGHTDVVISAAC-HPTENLIASAALENDKTIKLM 326 qq

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